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(54) **Title:** B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR IMMUNOMODULATION

(57) **Abstract:** The present invention provides nucleic acids encoding B7-related factors that modulate the activation of immune or inflammatory response cells, such as T-cells. Also provided are expression vectors and fusion constructs comprising nucleic acids encoding B7-related polypeptides, including BSL2 and splice variants thereof. The presnt invention further provides isolated B7-related polypeptides that are specifically reactive with B7-related polypeptides, or portions thereof. In addition, the present invention provides assays utilizing B7-related nucleic acids, polypeptides, fusion proctins, or antibodies that are useful for diagnostic applications and the immunomodulation of a human or animal subject.

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B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR IMMUNOMODULATION

FIELD OF THE INVENTION

The present invention relates to isolated nucleic acids encoding B7-related polypeptides, including BSL2 and splice variants, which modulate cells that are important for immune and inflammatory responses, such as T-cells. Also related are expression vectors and fusion constructs comprising nucleic acids encoding B7-related polypeptides. The present invention further relates to isolated B7-related polypeptides, isolated fusion proteins comprising B7-related polypeptides, and antibodies that are specifically reactive with B7-related polypeptides, or portions thereof. In addition, the present invention relates to methods of isolating and identifying the corresponding counter-receptor(s) of the B7-related polypeptides, utilizing B7-related polypeptides, or fusion proteins. Also related are methods of immunomodulation of a subject by the administration of compositions of the B7-related polypeptides, fusion proteins, cognate antibodies, or portions or derivatives thereof. The present invention further relates to methods of immunomodulation of animal or human subjects by the administration of compositions of genetically engineered vectors or host cells comprising the B7-related polypeptide expression cassettes as disclosed herein.

BACKGROUND OF THE INVENTION

The primary response of T-cells, involving T-cell activation, expansion, and differentiation is essential for the initiation of an immune response to a foreign antigen. The activation of T-cells by antigen presenting cells (APCs) requires at least two separate signals (K.E. Hellstrom et al. (1996) *Cancer Chemother. Pharmacol.* **38**:S40-1; N.K. Damle et al. (1992) *J. Immunol.* **148**:1985-92; J.M. Green et al. (1994) *Eur. J. Immunol.* **24**:265-72; E.C. Guinan et al. (1994) *Blood* **84**:3261-82; J.W. Hodge et al. (1995) *Cancer Res.* **55**:3598-603). The first signal causes T-cell entry into the cell cycle, and is mediated by foreign antigens presented by the major histocompatibility complex (MHC). The second signal, termed costimulation, causes cytokine production and T-cell proliferation, but is neither antigen-specific, nor MHC

restricted (R.H. Schwartz (1990) *Science* **248**:1349-1356).

Costimulation is believed to be mediated by one or more distinct cells surface molecules expressed by APCs (M.K. Jenkins et al. (1988) *J. Immunol.* **140**:3324-3330; P.S. Linsley et al. (1991) *J. Exp. Med.* **173**:721-730; C.D. Gimmi, et al. (1991) *Proc. Natl. Acad. Sci. USA* **88**:6575-6579; J.W. Young et al. (1992) *J. Clin. Invest.* **90**:229-237; L. Koulova et al. (1991) *J. Exp. Med.* **173**:759-762; H. Reiser et al. (1992) *Proc. Natl. Acad. Sci. USA* **89**:271-275; G.A. van-Seventer et al. (1990) *J. Immunol.* **144**:4579-4586; J. M. LaSalle et al. (1991) *J. Immunol.* **147**:774-80; M. I. Dustin et al. (1989) *J. Exp. Med.* **169**:503; R.J. Armitage et al. (1992) *Nature* **357**:80-82; Y. Liu et al. (1992) *J. Exp. Med.* **175**:437-445). Considerable evidence suggests that B7, an APC cell-surface protein, is one such costimulatory molecule (P.S. Linsley et al. (1991) *J. Exp. Med.* **173**:721-730; C.D. Gimmi et al. (1991) *Proc. Natl. Acad. Sci. USA* **88**:6575-6579; L. Koulova et al. (1991) *J. Exp. Med.* **173**:759-762; H. Reiser et al. (1992) *Proc. Natl. Acad. Sci. USA* **89**, 271-275; P.S. Linsley et al. (1990) *Proc. Natl. Acad. Sci. USA* **87**:5031-5035; G.J. Freeman et al. (1991) *J. Exp. Med.* **174**:625-631).

B7 has been shown to bind to two counter-receptors (ligands) expressed on T-cells, termed CD28 and CTLA-4. B7 binding to CD28 induces T-cells to proliferate and secrete IL-2 (P.S. Linsley et al. (1991) *J. Exp. Med.* 173, 721-730; C.D. Gimmi et al. (1991) *Proc. Natl. Acad. Sci. USA* **88**:6575-6579; C.B. Thompson et al. (1989) *Proc. Natl. Acad. Sci. USA* **86**:1333-1337; C.H. June et al. (1990) *Immunol. Today* **11**:211-6; F.A. Harding et al. (1992) *Nature* **356**:607-609), allowing full T-cell activation. Conversely, B7 binding to CTLA-4 mediates T-cell down-regulation. The importance of the B7:CD28/CTLA-4 costimulatory pathway has been demonstrated *in vitro* and in several *in vivo* model systems. Blockade of this pathway results in the development of antigen specific tolerance in murine and humans systems (F.A. Harding et al. (1992) *Nature* **356**:607-609; D.J. Lenschow et al. (1992) *Science* **257**:789-792; L.A. Turka et al. (1992) *Proc. Natl. Acad. Sci. USA* **89**:11102-11105; C.D. Gimmi et al. (1993) *Proc. Natl. Acad. Sci. USA* **90**:6586-6590). Conversely, the ectopic expression of B7 in

B7-negative murine tumor cells induces T-cell mediated specific immunity accompanied by tumor rejection and long lasting protection to tumor challenge (L. Chen et al. (1992) *Cell* **71**:1093-1102; S.E. Townsend et al. (1993) *Science* **259**:368-370; S. Baskar et al. (1993) *Proc. Natl. Acad. Sci. USA* **90**:5687-5690). Therefore, manipulation of the B7:CD28/CTLA-4 pathway offers great potential to stimulate or suppress immune responses in humans.

In addition to the previously characterized B7 molecule (referred to hereafter as B7-1) B7-1-like molecules have been identified (see, e.g., M. Azuma et al. (1993) *Nature* **366**:76-79; C. Chen et al. (1994) *J. Immunol.* **152**:4929-36; R.H. Reeves et al. (1997) *Mamm. Genome* **8**:581-582; K. Ishikawa et al. (1998) *DNA Res.* **5**:169-176; U.S. Patent No. 5,942,607 issued August 24, 1999 to Freeman et al.). In particular, PD-L1 and PD-L2 have been identified as inhibitors of T-cell activation (G.J. Freeman et al. (2000) *J. Exp. Med.* **192**:1027-1034; Y. Latchman et al., (2001) *Nature Immunology* **2**:261-268), whereas B7-H1, B7-H3, and B7-DC have been described as co-stimulators of T-cell proliferation (H. Dong et al. (1999) *Nature Medicine* **5**:1365-1369; A.I. Chapoval (2001) *Nature Immunology* **2**:269-274; Tseng et al. (2001) *J. Exp. Med.* **193**(7):839-45).

Thus, there is a growing family of factors related to B7-1, which modulate T-cell activation (reviewed by J. Henry et al. (1999) *Immunol. Today* **20**:285-288). The identification, isolation, and characterization of B7-related factors are therefore important goals for the further understanding of T-cell activation and function in both normal and disease states in animals, particularly humans. Accordingly, the present invention discloses the discovery and characterization of B7-related factors, including BSL2, and variants thereof. Also disclosed are various assays and treatments utilizing the BSL2 factors.

SUMMARY OF THE INVENTION

The present invention encompasses isolated nucleic acids encoding B7-related polypeptides that modulate inflammatory and immune responses, including T-cell activation (i.e., lymphokine production and/or T-

cell proliferation). B7-related polypeptides within the scope of the invention include counter-receptors on the surface of APCs capable of binding CD28/CTLA-4 and/or CD28-/CTLA-4-related ligand(s). Specifically, B7-related polypeptides include BSL2 polypeptides, and soluble fragments or derivatives thereof. More specifically, a B7-related nucleic acid is: i) a nucleic acid molecule comprising at least a fragment of a nucleotide sequence encoding a BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7); ii) a nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide that shares moderate to substantial sequence homology with a BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7); iii) a nucleic acid molecule capable of hybridizing to the BSL2 nucleotide sequences (e.g., **SEQ ID NO:**1, 2, 4, or 6), or fragments thereof, under appropriate conditions (e.g., moderate or high stringency hybridization conditions); iv) a nucleic acid molecule which differs from the nucleotide sequence of BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6) due to degeneracy in the genetic code, or recombinant or synthetic modifications; or v) a nucleic acid molecule that shares at least substantial homology with the BSL2 nucleic acid sequence (e.g., as set forth in **SEQ ID NO:**1, 2, 4, or 6).

In addition, nucleic acid probes or primers comprising B7-related sequences are encompassed by the present invention. Such probes and primers are useful, for example, for assaying a biological sample for the presence of APCs expressing a BSL2 factor.

The present invention also encompasses vectors (e.g., expression vectors) and fusion constructs comprising nucleic acids encoding B7-related polypeptides. Expression vectors direct the synthesis of the corresponding polypeptides or peptides in a variety of hosts, particularly eukaryotic cells, such as mammalian and insect cell culture, and prokaryotic cells, such as *Escherichia coli*. Expression vectors within the scope of the invention comprise a nucleic acid sequence encoding at least one B7-related polypeptide as described herein, and a promoter operatively linked to the nucleic acid sequence. In one embodiment, the expression vector comprises a DNA sequence encoding the extracellular domain of a BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7) fused to a DNA sequence encoding the Fc region

human immunoglobulin G1 (IgG1). Such expression vectors can be used to transform or transfect host cells to thereby produce polypeptides or peptides, including fusion proteins or peptides encoded by nucleic acid molecules as described herein.

The present invention further encompasses isolated B7-related polypeptides, including BSL2 polypeptides, or portions or derivatives thereof. Preferred B7-related polypeptides comprise the amino acid sequences of the BSL2 polypeptides (e.g., **SEQ ID NO:**3, 5, or 7), or portions thereof. Such polypeptides comprise at least a portion of the mature forms of the BSL2 polypeptides, and preferably comprise soluble forms of these polypeptides. Also encompassed by the present invention are polypeptides that share moderate to substantial homology with the amino acid sequence of the invention (e.g., as set forth in **SEQ ID NO:**3, 5, or 7) which are naturally occurring isoforms of the BSL2 polypeptides, or modified recombinant polypeptides.

The present invention additionally encompasses isolated fusion proteins comprising the B7-related polypeptides, or portions or derivatives thereof, as disclosed herein. In one aspect, the fusion protein comprises an extracellular domain portion of a B7-related polypeptide fused to another polypeptide that alters the solubility, purification, binding affinity, and/or valency of the B7-related polypeptide. Preferably, a DNA molecule encoding an extracellular domain portion of the BSL2 polypeptides can be joined to DNA encoding the Fc region of human IgG1 to form DNA fusion products that encode the BSL2-Ig (e.g., **SEQ ID NO:**9, 11, or 13), or fusion proteins.

Further, the present invention encompasses methods of isolating and identifying the corresponding counter-receptor(s) of the B7-related polypeptides, utilizing the isolated B7-related polypeptides, fusion proteins, or cognate antibodies disclosed herein. In one embodiment, isolated BSL2 polypeptides, or portions thereof, can be incubated with protein extracts obtained from immune or inflammatory response cells, such as T-cells, to form a BSL/receptor complex, and then incubated with anti-BSL antibodies to isolate the BSL/receptor complex. Alternatively, a fusion protein comprising

the BSL2 polypeptide can be incubated with protein extracts obtained from immune or inflammatory response cells, such as T-cells, and then incubated with antibodies that specifically react with the fusion protein. Receptors that bind to the B7-related polypeptides would be expected to have significant immunomodulatory activity.

The present invention also encompasses diagnostic methods and kits utilizing the B7-related factors of the present invention, including nucleic acids, polypeptides, antibodies, or functional fragments thereof. Such factors can be used, for example, in diagnostic methods and kits for measuring expression levels of B7-related factors, and to screen for various B7-related diseases. In addition, the B7-related nucleic acids described herein can be used to identify chromosomal abnormalities affecting BSL2, and to identify allelic variants or mutations of BSL2 in an individual or population.

In addition, the present invention encompasses isolated antibodies, including monoclonal and polyclonal antibodies, that are specifically reactive with the B7-related polypeptides, fusion proteins, or portions or derivatives thereof, as disclosed herein. Preferably, monoclonal antibodies are prepared to be specifically reactive with the BSL2 polypeptides (e.g., **SEQ ID NO:**3, 5, or 7), or portions or derivatives thereof.

The present invention further encompasses methods of immunomodulation of a human or animal subject by the administration of compositions of the B7-related polypeptides, fusion proteins, or portions or derivatives thereof, as disclosed herein. Such compositions would be expected to up-regulate or down-regulate the activities of immune or inflammatory response cells (e.g., T-cells). For example, B7-related polypeptides in a composition may interact with CD28 and thereby up-regulate immune cell activity. Alternatively, B7-related polypeptides in a composition may interact with CTLA-4 and thereby down-regulate immune cell activity. In one embodiment, compositions of BSL2-Ig fusion proteins are administered, e.g. via injection, to a subject to provide systemic immunosupression or immunostimulation. In a specific embodiment, BSL2-Ig (e.g., **SEQ ID NO:**9, 11, or 13) fusion proteins can be used to inhibit T-cell

proliferation, and thereby treat conditions associated with aberrant or increased T-cell proliferation. The protein or fusion protein compositions of the invention can be administered alone, or in combination with one or more immunomodulatory molecules. For example, BSL2-Ig fusion proteins (e.g., **SEQ ID NO:**9, 11, or 13) can be administered in combination with antibodies against a BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7) to inhibit T-cell proliferation.

Also encompassed by the present invention are methods of immunomodulation of a human or animal subject by the administration of compositions of antibodies that are specifically reactive with the B7-related polypeptides, fusion proteins, or portions or derivatives thereof, as disclosed herein. Such compositions can be expected to block the co-stimulatory activities of the B7-related polypeptides, and to down-regulate immune or inflammatory response cells (e.g., T-cells), accordingly. In one embodiment, compositions of monoclonal antibodies that are specifically reactive with the BSL2 polypeptides (e.g., **SEQ ID NO:**3, 5, or 7), or fragments thereof, are administered, e.g., via injection, to a subject to provide immunosupression or induced tolerance. In a specific embodiment, monoclonal antibodies against a BSL2 polypeptide (e.g., **SEQ ID NO:**3) can be used to inhibit T-cell proliferation, and thereby treat conditions associated with aberrant or increased T-cell proliferation. Antibody compositions can be administered alone, or in combination with one or more immunomodulatory molecules. For example, antibodies against a BSL2 polypeptide (e.g., **SEQ ID NO:**3) can be administered in combination with a BSL2-Ig fusion protein (e.g., **SEQ ID NO:**9) to inhibit T-cell proliferation. The methods of inducing tolerance described herein can be used prophylactically for preventing immune responses such as transplantation rejection (solid organ and bone marrow) and graft versus host disease, especially in autologous bone marrow transplantation. Such methods can also be useful therapeutically, in the treatment of autoimmune diseases, transplantation rejection, and established graft versus host disease in a subject.

The present invention additionally encompasses methods of the

immunomodulation of a human or animal subject by the administration of compositions of genetically engineered vectors or cells comprising the B7-related polypeptide expression cassettes as disclosed herein. In a preferred embodiment, the cells are antigen presenting cells, such as a macrophages, which are transfected or transduced to allow expression of one or more of the B7-related polypeptides, including the BSL2 polypeptides (e.g., **SEQ ID NO:**3, 5, or 7), fusion proteins, or fragments or derivatives thereof, and then introduced e.g., via transplantation, into the recipient. Consistent with the present invention, the genes encoding the BSL2 polypeptides or fusion proteins can be transfected or transduced alone, or in combination with genes encoding other immunomodulatory molecules.

Additional objects and advantages afforded by the present invention will be apparent from the detailed description and exemplification herein below.

BRIEF DESCRIPTION OF THE FIGURES

The appended drawings of the figures are presented to further describe the invention and to assist in its understanding through clarification of its various aspects. In the figures of the present invention, the nucleotide and amino acid sequences are represented by their one-letter abbreviations.

Figures 1A-1C, 2A-2B, and **3A-3C** illustrate the nucleotide and predicted amino sequences of the BSL2 clones. **Figure 1A** shows the nucleotide sequence of the BSL2-4616811 clone (**SEQ ID NO:**1); nucleotides 1-12 include vector sequence; nucleotides 121-123 contain the translation initiation signal (ATG); between nucleotides 204-205 is the predicted signal peptide cleavage site; nucleotides 1516-1587 encode the predicted transmembrane domain; nucleotides 1723-1725 contain the translation termination signal (TGA). **Figure 1B** shows the coding sequence of BSL2-4616811 (BSL2vcvc; **SEQ ID NO:**2). The sequence encoding the mature form of the BSL2-4616811 polypeptide begins at nucleotide 85; nucleotides 1-3 contain the translation initiation signal (ATG); and nucleotides 1396-1467 encode the predicted transmembrane domain. **Figure 1C** shows the predicted amino acid sequence of the BSL2-4616811 clone (**SEQ ID NO:**3);

amino acids 1-465 contain the predicted ECD. The sequence of the mature BSL2-4616811 polypeptide begins at amino acid 29. It is noted that BSL2-4616811 is also called BSL2vcvc for the purposes of this invention.

Figure 2A shows the nucleotide sequence of the BSL2-L165-21 clone (**SEQ ID NO:**4); nucleotides 1-3 contain the translation initiation signal (ATG); between nucleotides 84-85 is the predicted signal peptide cleavage site; nucleotides 742-813 encode the predicted transmembrane domain; nucleotides 949-951 contain the translation termination signal (TGA). **Figure 2B** shows the predicted amino acid sequence of the BSL2-L165-21 clone (**SEQ ID NO:**5); amino acids 1-247 contain the predicted ECD. It is noted that BSL2-L165-21 is also called BSL2v2c2 for the purposes of this invention.

Figure 3A shows the nucleotide sequence of the BSL2-L165-35b clone (**SEQ ID NO:**6); nucleotides 1-3 contain the translation initiation signal (ATG); between nucleotides 84-85 is the predicted signal peptide cleavage site; nucleotides 742-813 encode the predicted transmembrane domain; nucleotides 949-951 contain the translation termination signal (TGA). The sequence encoding the mature BSL2-L165-35b polypeptide begins at nucleotide 85. **Figure 3B** shows the predicted amino acid sequence of the BSL2-L165-35b clone (**SEQ ID NO:**7); amino acids 1-247 contain the predicted ECD. The sequence encoding the mature BSL2-L165-35b polypeptide begins at amino acid 29. It is noted that BSL2-L165-35b is also called BSL2v1c2 for the purposes of this invention. **Figure 3C** shows the exons and alternative splicing diagram for the BSL2 clones, including BSL2-4616811 (BSL2vcvc), BSL2-L165-21 (BSL2v2c2), and BSL2-L165-35b (BSL2v1c2). In the diagram, the exons are not drawn to scale, and the first 66 nucleotides of the BSL2-4616811 clone are not mapped to the genomic sequence.

Figures 4A-4B, 5A-5B, and **6A-6B** illustrate the nucleotide and predicted amino sequences of the BSL2-4616811-Ig (BSL2vcvc-Ig), BSL2-L165-35b-Ig (BSL2v1c2-Ig), and BSL2-L165-21-Ig (BSL2v2c2-Ig) fusion constructs. **Figure 4A** shows the nucleotide sequence of the BSL2-4616811-Ig clone (**SEQ ID NO:**8); nucleotides 1-3 contain the translation initiation

signal (ATG); nucleotides 1-1394 encode the BSL2-4616811 ECD; nucleotide 1395 is a silent mutation introduced to facilitate construction of the fusion protein; nucleotides 1396-2094 encode the Fc portion of human IgG1; nucleotides 2095-2097 contain the translation termination signal (TGA).

Figure 4B shows the predicted amino acid sequence of the BSL2-4616811-Ig fusion protein (**SEQ ID NO:9**); amino acids 1-465 of contain the BSL2-4616811 ECD; amino acids 85-465 contain the mature BSL2-4616811 ECD; amino acids 466-698 contain the Fc domain of human IgG.

Figure 5A shows the nucleotide sequence of the BSL2-L165-35b-Ig clone (**SEQ ID NO:10**); nucleotides 1-3 contain the translation initiation signal (ATG); nucleotides 1-84 encode the predicted signal peptide sequence; nucleotides 85-738 encode the mature ECD; nucleotides 739-744 contain a restriction site introduced by PCR to facilitate construction of the fusion; and nucleotides 745-1440 encode the human Ig portion of the fusion construct. **Figure 5B** shows the predicted amino acid sequence of the BSL2-L165-35b-Ig fusion protein (**SEQ ID NO:11**); amino acids 1-28 contain the predicted signal peptide sequence; amino acids 29-226 contain the mature ECD; amino acids 227-228 correspond to the restriction site introduced by PCR; amino acids 229-480 contain the human Ig portion of the fusion.

Figure 6A shows the nucleotide sequence of the BSL2-L165-21-Ig clone (**SEQ ID NO:12**); nucleotides 1-3 contain the translation initiation signal (ATG); nucleotides 1-84 encode the predicted signal peptide sequence; nucleotides 85-738 encode the predicted mature ECD; nucleotides 739-744 contain an *Eco*RI site introduced by PCR to facilitate construction of the fusion; nucleotides 745-1440 encode the human Ig portion of the fusion construct. **Figure 6B** shows the predicted amino acid sequence of the BSL2-L165-21-Ig fusion protein (**SEQ ID NO:13**); amino acid 1 is the initiating methionine; amino acids 1-28 contain the predicted signal peptide sequence; amino acids 29-246 contain the predicted mature ECD; amino acids 247-248 correspond to the *Eco*RI restriction site introduced by PCR; amino acids 249-480 contain the human Ig portion of the fusion protein.

Figures 7A-7B illustrate the reagents and results of expression

analysis performed for BSL2. **Figure 7A** shows the nucleotide sequence of the BSL2 probe (**SEQ ID NO:**14). **Figure 7B** shows the levels of BSL2 mRNA observed in various cell types as determined by Northern blot analysis; "PBT" indicates peripheral blood T-cells; "CD3/CD28" indicates stimulation with anti-CD3 and anti-CD28 antibodies; "PMA" indicates stimulation with phorbol 12 myristate 13 acetate; "LPS" indicates stimulation with lipopolysaccharide; "PBM" indicates peripheral blood monocytes; "PHA" indicates stimulation with phytohemaglutinin; "GM-CSF/IL-4" indicates stimulation with GM-CSF and IL-4; "HMVEC" indicates human microvascular endothelial cells; "TNF-alpha" indicates stimulation with TNF-alpha; and "H292 (Starved) indicates serum starved H292 cells.

Figures 8A-8E illustrate the results of PCR analysis performed to determine the relative levels of the BSL2-4616811 (BSL2vcvc) or BSL2-L165-35b (BSL2v1c2) transcripts in various cell types, with or without stimulation. The top arrow points to the bands representing the BSL2-4616811 transcript; the bottom arrow points to the bands representing the BSL2-L165-35b transcript. **Figure 8A** shows the results for RAJI, RAMOS, PM-LCL, and PL-LCL cell types, with or without PMA and ionomycin stimulation. **Figure 8B** shows the results for CE-LCL cells, HL60, Thp1, and HUVEC cell types, with or without stimulation. **Figure 8C** shows the results for peripheral blood T-cells with or without PMA and ionomycin stimulation. The results from cells isolated from two separate donors are shown (donor 079 and donor 124). **Figure 8D** shows the results for CEM and HUT78 cells, with or without PMA and ionomycin stimulation. **Figure 8E** shows the results of a PCR reaction using BSL2-4616811 plasmid as template. Lane 1: Lambda *Bst*EII DNA ladder; lane 2: PCR product. The results demonstrate that the forward primer preferentially binds the specific binding site in the first variable fold rather than for the homologous site in the second variable fold of BSL2-4616811.

Figure 9 illustrates the results of fluorescence activated cell sorting (FACS) analysis of A549 epithelial lung cells using anti-BSL2-4616811 MAb. Column 1: no MAb; column 2: isotype control; column 3: anti-BSL2

MAb 1F7G2; column 4: anti-BSL2 MAb 2B10D7; column 5: anti-BSL2 MAb 3E6D3; column 6: anti-BSL2 MAb 4C2C6; column 7: anti-BSL2 MAb 5D7E2.

Figures 10A-10J illustrate suppression of peripheral blood T-cell proliferation using BSL2-4616811-Ig (BSL2vcvc-Ig) and/or anti-BSL2 MAb. **Figure 10A** shows results obtained using decreasing concentrations of anti-CD3 MAb, and constant concentrations of BSL2-4616811-Ig (BSL2vcvc-Ig) or ChiL6 fusion proteins. **Figure 10B** shows results obtained using a constant concentration of anti-CD3 MAb, and decreasing concentrations of BSL2-4616811-Ig (BSL2vcvc-Ig) or ChiL6 fusion proteins. **Figure 10C** shows results obtained using a decreasing concentration of anti-CD28 MAb, a constant concentration of anti-CD3 MAb, and a constant concentration of BSL2-4616811-Ig (BSL2vcvc-Ig) or ChiL6 fusion proteins. **Figure 10D** shows results obtained using a constant concentration of anti-CD3 MAb, a decreasing concentration of BSL2-4616811-Ig (BSL2vcvc-Ig), BSL2-L165-35b-Ig (BSL2v1c2-Ig), or ChiL6 fusion proteins. In the graph, "BSL2vcIg" represents BSL2-L165-35b-Ig (BSL2v1c2-Ig). **Figure 10E** shows results obtained using a constant concentration of anti-CD3 MAb, a constant concentration of BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein, and decreasing concentrations of anti-BSL2-1 MAb, anti-BSL2-5 MAb, or non-specific 3_15 MAb. **Figure 10F** shows results obtained using a constant concentration of anti-CD3 MAb, a constant concentration of BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein, and decreasing concentrations of anti-BSL2-1 MAb, anti-BSL2-2 MAb, anti-BSL2-3 MAb, anti-BSL2-4 MAb, BSL2-5 MAb, or non-specific 3_15 MAb. **Figure 10G** shows results obtained using a constant concentration of anti-CD3 MAb, a constant concentration of ChiL6 fusion protein, and decreasing concentrations of anti-BSL2-1 MAb or non-specific 3_15 MAb, or no MAb. **Figure 10H** shows results obtained using a constant concentration of anti-CD3 MAb, a constant concentration of BSL2-L165-35b-Ig (BSL2v1c2-Ig) fusion protein, and decreasing concentrations of anti-BSL2-1 MAb or non-specific 3_15 MAb, or no MAb. **Figure 10I** shows results obtained using a constant concentration of anti-CD3 MAb, followed by a constant concentration of BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein,

later followed by decreasing concentrations of plate-bound anti-BSL2-1 MAb or non-specific 3_15 MAb, or no MAb. In this experiment, MAb was bound to the plate after addition of BSL2-4616811-Ig (BSL2vcvc-Ig). **Figure 10J** shows results obtained using a constant concentration of anti-CD3 MAb, followed by decreasing concentrations of plate-bound anti-BSL2-1 MAb, non-specific 3_15 MAb, or no MAb, later followed by a constant concentration of BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein. In this experiment, MAb was bound to the plate before addition of BSL2-4616811-Ig (BSL2vcvc-Ig).

Figures 11A-11B illustrate results obtained from mixed lymphocyte reactions. **Figure 11A** shows reactions from cells incubated with decreasing concentrations of BSL2-4616811-Ig (BSL2vcvc-Ig), CTLA-4-Ig, or ChiL6 fusion proteins. In the graph, "(124 X 051)" indicates that T-cells from donor 124 were used as responders and monocytes from donor 051 were used as stimulators for the reactions. **Figure 11B** shows reactions from cells incubated with BSL2-4616811-Ig (BSL2vcvc-Ig), BSL2-L165-35b-Ig (BSL2v1c2-Ig), or ChiL6 fusion proteins. In the graph, "BSL2vcIg" represents BSL2-L165-35b-Ig (BSL2v1c2-Ig) fusion protein; and "(82 X 148)" indicates that T-cells from donor 82 were used as responders and monocytes from donor 148 were used as stimulators for the reactions.

Figure 12 shows the results of a binding comparison of anti-BSL2 MAb to BSL2-4616811-Ig (BSL2vcvc-Ig) and BSL2v1c2-Ig. In the graph, "vcvc" represents BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein; "vc" represents BSL2-L165-35b-Ig (BSL2v1c2-Ig) fusion protein.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the methods of the present invention, three B7-related factors, designated BSL2, have been identified and characterized. In addition, three distinct BSL2 splice variants have been identified, including BSL2-4616811 (BSL2vcvc), BSL2-L165-21 (BSL2v2c2), and BSL2-L165-35b (BSLv1c2). These B7-related factors may provide a molecular basis for the activation of immune or inflammatory response cells, such as T-cells, at different times and in different illnesses and disease states. In addition, the disclosed B7-related factors can be utilized in the prevention or treatment

certain diseases by modulating the activity of immune or inflammatory response cells, such as T-cells, using the methods described in detail herein. These methods can be used as prophylaxis or treatments for cancers or immune-related disorders as detailed below.

Notably, experiments described herein demonstrate that BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein acts synergistically with anti-BSL2 MAbs to inhibit T-cell proliferation. Accordingly, compositions comprising BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein may be used alone or in conjunction with compositions comprising anti-BSL2 MAbs for treatments of various disorders, including acute and chronic transplant rejection, rheumatoid arthritis, multiple sclerosis, psoriasis, or other diseases described in detail herein. In addition, such compositions can be used individually or in combination for therapeutic applications such as xenotransplantation.

B7-related nucleic acids

One aspect of the present invention pertains to isolated nucleic acids having a nucleotide sequence such as BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6), or fragments or complementary sequences thereof. The nucleic acid molecules of the invention can be DNA or RNA. A preferred nucleic acid is a DNA encoding the human BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7), or fragments or functional equivalents thereof. Such nucleic acids can comprise at least 15, 20, 25, 50, 60, 100, 200, 240, 255, 270, 300, 305, 310, 410, 500, 619, 630, 700, or 1000 contiguous nucleotides.

The term "isolated" as used throughout this application refers to a B7-related nucleic acid, polypeptide, peptide, protein fusion, or antibody, that is substantially free of cellular material or culture medium. An isolated or substantially purified molecule contains less than about 50%, preferably less than about 25%, and most preferably less than about 10%, of the cellular components with which it was associated.

The term "functional equivalent" is intended to include nucleotide sequences encoding functionally equivalent B7-related factors. A functional equivalent of a B7-related protein includes fragments or variants that perform at least one characteristic function of the B7-related protein (e.g., ligand-

binding, antigenic, intra-, or intercellular activity). For example, DNA sequence polymorphisms within the nucleotide sequence of a B7-related factor, especially those within the third base of a codon, may result in "silent" mutations, which do not affect the encoded amino acid sequence of the protein due to the degeneracy of the genetic code.

In one embodiment, the present invention encompasses a polynucleotide comprising the start codon and the remaining coding sequence of BSL2-4616811 (BSL2vcvc). Specifically, the invention encompasses a polynucleotide comprising nucleotides 1 through 1602 of **SEQ ID NO:**2. The invention also encompasses a polynucleotide comprising nucleotides 121 through 1722 of **SEQ ID NO:**1, and the corresponding polypeptide comprising amino acids 1 through 534 of **SEQ ID NO:**3. Also encompassed are vectors comprising these polynucleotides, and host cells comprising these vectors.

In another embodiment, the present invention embraces a polynucleotide lacking the initiating start codon, but including the remaining coding sequence of BSL2-4616811 (BSL2vcvc). Specifically, the invention embraces a polynucleotide comprising nucleotides 4 through 1602 of **SEQ ID NO:**2. In addition, the invention embraces a polynucleotide comprising nucleotides 124 through 1722 of **SEQ ID NO:**1, and the polypeptide corresponding to amino acids 2 through 534 of **SEQ ID NO:**3. Also embraced are vectors comprising these polynucleotides, and host cells comprising these vectors.

The present invention also encompasses a polynucleotide comprising the start codon and the remaining coding sequence of BSL2-L165-35b (BSL2v1c2). Specifically, the invention encompasses a polynucleotide comprising nucleotides 1 through 948 of **SEQ ID NO:**6. The invention further encompasses a corresponding polypeptide comprising amino acids 1 through 316 of **SEQ ID NO:**7. Also encompassed are vectors comprising these polynucleotides, and host cells comprising these vectors.

The present invention also embraces a polynucleotide lacking the initiating start codon, but including the remaining coding sequence of BSL2-L165-35b (BSL2v1c2). Specifically, the invention embraces a

polynucleotide comprising nucleotides 4 through 948 of **SEQ ID NO:**6. In addition, the invention embraces a polypeptide corresponding to amino acids 2 through 316 of **SEQ ID NO:**7. Also embraced are vectors comprising these polynucleotides, and host cells comprising these vectors.

The invention further encompasses a polynucleotide comprising the start codon and the remaining coding sequence of BSL2-L165-21 (BSL2v2c2). Specifically, the invention encompasses a polynucleotide comprising nucleotides 1 through 948 of **SEQ ID NO:**4. The invention further encompasses a corresponding polypeptide comprising amino acids 1 through 316 of **SEQ ID NO:**5. Also encompassed are vectors comprising these polynucleotides, and host cells comprising these vectors.

The present invention further embraces a polynucleotide lacking the initiating start codon, but including the remaining coding sequence of BSL2-L165-21 (BSL2v2c2). Specifically, the invention embraces a polynucleotide comprising nucleotides 4 through 948 of **SEQ ID NO:**4. In addition, the invention embraces a polypeptide corresponding to amino acids 2 through 316 of **SEQ ID NO:**5. Also embraced are vectors comprising these polynucleotides, and host cells comprising these vectors.

Preferred embodiments include an isolated nucleic acid sharing at least 60, 70, 80, 85, 90, 95, 97, 98, 99, 99.5, or 100% sequence identity with a polynucleotide sequence of BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6), or a complementary sequence thereof. This polynucleotide sequence may be identical to the nucleotide sequence of BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6, or complementary sequences), or may include up to a certain integer number of nucleotide alterations as compared to the reference sequence.

"Identity," as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, "identity" also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. "Identity" and "similarity" can be readily calculated by known methods, including but not limited to those described in (*Computational*

Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; *Biocomputing. Informatics and Genome Projects*, Smith, D. W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D. (1988) *SIAM J. Applied Math.*, **48**:1073.

For nucleic acids, sequence identity can be determined by comparing a query sequences to sequences in publicly available sequence databases (NCBI) using the BLASTN2 algorithm (S.F. Altschul et al. (1997) *Nucl. Acids Res.*, **25**:3389-3402). The parameters for a typical search are: E = 0.05, v = 50, B = 50, wherein **E** is the expected probability score cutoff, V is the number of database entries returned in the reporting of the results, and B is the number of sequence alignments returned in the reporting of the results (S.F. Altschul et al. (1990) *J. Mol. Biol.*, **215**:403-410).

In another approach, nucleotide sequence identity can be calculated using the following equation: % identity = (number of identical nucleotides) / (alignment length in nucleotides) * 100. For this calculation, alignment length includes internal gaps but not terminal gaps. Alternatively, nucleotide sequence identity can be determined experimentally using the specific hybridization conditions described below.

In accordance with the present invention, nucleic acid alterations are selected from the group consisting of at least one nucleotide deletion, substitution, including transition and transversion, insertion, or modification (e.g., via RNA or DNA analogs, dephosphorylation, methylation, or labeling). Alterations may occur at the 5' or 3' terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among the nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence. Alterations of a nucleic acid sequence of BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6)

may create nonsense, missense, or frameshift mutations in the coding sequence, and thereby alter the polypeptide encoded by the nucleic acid.

Also encompassed by the present invention are splice variants derived from the BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6) nucleic acid sequences. As used herein, the term "splice variant" refers to variant B7-related nucleic acids and polypeptides produced by differential processing of the primary transcript(s) of genomic DNA. An alternate splice variant may comprise, for example, any one of the sequences of BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6) disclosed herein. Alternate splice variants can also comprise other combinations of introns/exons of BSL2, which can be determined by those of skill in the art. Alternate splice variants can be determined experimentally, for example, by isolating and analyzing cellular RNAs (e.g., Southern blotting or PCR), or by screening cDNA libraries using the B7-related nucleic acid probes or primers described herein. In another approach, alternate splice variants can be predicted using various methods, computer programs, or computer systems available to practitioners in the field.

General methods for splice site prediction can be found in Nakata (1985) *Nucleic Acids Res.* **13**:5327-5340. In addition, splice sites can be predicted using, for example, the GRAIL™ (E.C. Uberbacher and R.J. Mural (1991) *Proc. Natl. Acad. Sci. USA*, **88**:11261-11265; E.C. Uberbacher (1995) *Trends Biotech.*, **13**:497-500; GenView (L. Milanesi et al. (1993) *Proceedings of the Second International Conference on Bioinformatics, Supercomputing, and Complex Genome Analysis*, H.A. Lim et al. (eds), World Scientific Publishing, Singapore, pp. 573-588; SpliceView; and HSPL (V.V. Solovyev et al. (1994) *Nucleic Acids Res.* **22**:5156-5163; V.V. Solovyev et al. (1994) "The Prediction of Human Exons by Oligonucleotide Composition and Discriminant Analysis of Spliceable Open Reading Frames," R. Altman et al. (eds), *The Second International conference on Intelligent systems for Molecular Biology*, AAAI Press, Menlo Park, CA, pp. 354-362; V.V. Solovyev et al. (1993) "Identification Of Human Gene Functional Regions Based On Oligonucleotide Composition," L. Hunter et al. (eds), *In Proceedings of First*

International conference on Intelligent System for Molecular Biology, Bethesda, pp. 371-379) computer systems.

Additionally, computer programs such as GeneParser (E.E. Snyder and G.D. Stormo (1995) *J. Mol. Biol.* **248**: 1-18; E.E. Snyder and G.D. Stormo (1993) *Nucl. Acids Res.* **21**(3): 607-613; MZEF (M.Q. Zhang (1997) *Proc. Natl. Acad. Sci. USA*, **94**:565-568; MORGAN (S. Salzberg et al. (1998) *J. Comp. Biol.* **5**:667-680; S. Salzberg et al., eds. (1998) *Computational Methods in Molecular Biology*, Elsevier Science, New York, NY, pp. 187-203); VEIL (J. Henderson et al. (1997) *J. Comp. Biol.* **4**:127-141); GeneScan (S. Tiwari et al. (1997) *CABIOS (BioInformatics)* **13**: 263-270); GeneBuilder (L. Milanesi et al. (1999) *Bioinformatics* **15**:612-621); Eukaryotic GeneMark (J. Besemer et al. (1999) *Nucl. Acids Res.* **27**:3911-3920); and FEXH (V.V. Solovyev et al. (1994) *Nucl. Acids Res.* **22**:5156-5163) can be used. In addition, splice sites (i.e., former or potential splice sites) in cDNA sequences can be predicted using, for example, the RNASPL (V.V. Solovyev et al. (1994) *Nucl. Acids Res.* **22**:5156-5163); or INTRON (A. Globek et al. (1991) INTRON version 1.1 manual, Laboratory of Biochemical Genetics, NIMH, Washington, D.C.) programs.

The present invention also encompasses naturally-occurring polymorphisms of BSL2 (e.g., **SEQ ID NO:1**, 2, 4, or 6), or sequences complementary thereto. As will be understood by those in the art, the genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution generating variant forms of gene sequences (Gusella (1986) *Ann. Rev. Biochem.* **55**:831-854). Restriction fragment length polymorphisms (RFLPs) include variations in DNA sequences that alter the length of a restriction fragment in the sequence (Botstein et al. (1980) *Am. J. Hum. Genet.* **32**, 314-331. RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; WO 90/11369; Donis-Keller (1987) *Cell* **51**:319-337; Lander et al. (1989) *Genetics* **121**: 85-99). Short tandem repeats (STRs) include tandem di-, tri- and tetranucleotide repeated motifs, also termed variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (U.S. Pat. No.

5,075,217; Armour et al. (1992) *FEBS Lett.* **307**:113-115; Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Single nucleotide polymorphisms (SNPs) are far more frequent than RFLPS, STRs, and VNTRs. SNPs may occur in protein coding (e.g., exon), or non-coding (e.g., intron, 5'UTR, 3'UTR) sequences. SNPs in protein coding regions may comprise silent mutations that do not alter the amino acid sequence of a protein. Alternatively, SNPs in protein coding regions may produce conservative or non-conservative amino acid changes, described in detail below. In some cases, SNPs may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. SNPs within protein-coding sequences can give rise to genetic diseases, for example, in the β-globin (sickle cell anemia) and CFTR (cystic fibrosis) genes. In non-coding sequences, SNPs may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms tend to occur with greater frequency and are typically spaced more uniformly throughout the genome than other polymorphisms. Also, different SNPs are often easier to distinguish than other types of polymorphisms (e.g., by use of assays employing allele-specific hybridization probes or primers). In one embodiment of the present invention, a BSL2 (e.g., **SEQ ID NO:1**, 2, 4, or 6) nucleic acid contains at least one SNP. Various combinations of these SNPs are also encompassed by the invention. In a preferred aspect, a B7-related SNP is associated with a immune system disorder, such as the disorders described in detail herein.

Further encompassed by the present invention are nucleic acid molecules that share moderate homology with the BSL2 nucleic acid sequences (e.g., **SEQ ID NO:1**, 2, 4, or 6) or complementary sequences, and hybridize to these sequences under moderate stringency hybridization conditions. More preferred are nucleic acid molecules that share substantial

homology with these sequences and hybridize under high stringency hybridization conditions. As used herein, the phrase "moderate homology" refers to sequences which share at least 60% sequence identity with a reference sequence (e.g., SEQ ID NO:1, 2, 4, or 6, or complementary sequences), whereas the phrase "substantial homology" refers to sequences that share at least 90% sequence identity with a reference sequence. It is recognized, however, that polypeptides and the nucleic acids encoding such polypeptides containing less than the above-described level of homology arising as splice variants or that are modified by conservative amino acid substitutions (or substitution of degenerate codons) are contemplated to be within the scope of the present invention.

The phrase "hybridization conditions" is used herein to refer to conditions under which a double-stranded nucleic acid hybrid is formed from two single nucleic acid strands, and remains stable. As known to those of skill in the art, the stability of the hybrid sequence is reflected in the melting temperature (T_m) of the hybrid (see F.M. Ausubel et al., Eds, (1995) *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc., New York, NY). The T_m decreases approximately 0.5°C to 1.5°C with every 1% decrease in sequence homology. In general, the stability of a hybrid sequence is a function of the length and guanine/cytosine content of the hybrid, the sodium ion concentration, and the incubation temperature. Typically, the hybridization reaction is initially performed under conditions of low stringency, followed by washes of varying, but higher, stringency. Reference to hybridization stringency relates to such washing conditions.

In accordance with the present invention, "high stringency" conditions can be provided, for example, by hybridization in 50% formamide, 5 X Denhardt's solution, 5 X SSPE, and 0.2% SDS at 42°C., followed by washing in 0.1 X SSPE and 0.1% SDS at 65°C. By comparison, "moderate stringency" can be provided, for example, by hybridization in 50% formamide, 5 X Denhardt's solution, 5 X SSPE, and 0.2% SDS at 42°C, followed by washing in 0.2 X SSPE and 0.2% SDS at 65°C. In addition, "low stringency" conditions can be provided, for example, by hybridization in 10% formamide,

5 X Denhardt's solution, 6 X SSPE, and 0.2% SDS at 42°C, followed by washing in 1 X SSPE and 0.2% SDS at 50°C. It is understood that these conditions may be varied using a variety of buffers and temperatures well known to those skilled in the art.

In a preferred embodiment of the present invention, the nucleic acid is a DNA molecule encoding at least a portion of the B7-related factor. A nucleic acid molecule encoding a novel B7-related factor can be obtained from mRNA present in activated B lymphocytes. It may also be possible to obtain nucleic acid molecules encoding B7-related factors from B cell genomic DNA. Thus, a nucleic acid encoding a B7-related factor can be cloned from either a cDNA or a genomic library in accordance with the protocols described in detail herein. Nucleic acids encoding novel B7-related factors can also be cloned from genomic DNA or cDNA using established polymerase chain reaction (PCR) techniques (see K. Mullis et al. (1986) *Cold Spring Harbor Symp. Quant. Biol.* **51**:260; K.H. Roux (1995) *PCR Methods Appl.* **4**:S185) in accordance with the nucleic acid sequence information provided herein. The nucleic acid molecules of the invention, or fragments thereof, can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (see, for example, U.S. Patent No. 4,598,049 to Itakura et al.; U.S. Patent No. 4,458,066 to Caruthers et al.; U.S. Patent Nos. 4,401,796 and 4,373,071 to Itakura).

It will be appreciated by one skilled in the art that variations in one or more nucleotides (up to about 3-4% of the nucleotides) of the nucleic acid molecules encoding novel B7-related factors may exist among individuals within a population due to natural allelic variation. Any and all such nucleotide variations and resulting amino acid polymorphisms are within the scope of the invention. Furthermore, there may be one or more isoforms or related, cross-reacting family members of the B7-related factors described herein. Such isoforms or family members are defined as polypeptides that are related in function and amino acid sequence to a B7-related factor (e.g., BSL2), but

encoded by genes at different loci. In addition, it is possible to modify the DNA sequence of B7-related factors using genetic techniques to produce proteins or peptides with altered amino acid sequences.

DNA sequence mutations can be introduced into a nucleic acid encoding a B7-related factor by any one of a number of methods, including those for producing simple deletions or insertions, systematic deletions, insertions or substitutions of clusters of bases or substitutions of single bases, to generate desired variants. Mutations of the B7-related nucleic acid molecule to generate amino acid substitutions or deletions are preferably obtained by site-directed mutagenesis. Site directed mutagenesis systems are well known in the art, and can be obtained from commercial sources (see, for example, Amersham Pharmacia Biotech, Inc., Piscataway, NJ). Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, DNASTAR software (DNASTAR, Inc., Madison, WI). Mutant forms of the BSL2 nucleic acid molecules (e.g., **SEQ ID NO:1**, 2, 4, or 6, or complementary sequences) are considered within the scope of the present invention, where the expressed polypeptide or peptide is capable modulating the activity and/or proliferation of immune or inflammatory cells (e.g., T-cells).

A fragment of the nucleic acid molecule encoding a novel B7-related factor is defined as a nucleotide sequence having fewer nucleotides than the nucleotide sequence encoding the entire amino acid sequence of the B7-related factor. Nucleic acid fragments which encode polypeptides which retain the ability to bind to their natural ligand(s) on immune or inflammatory response cells, such as T-cells, and either amplify or block immune responses (as evidenced by, for example, lymphokine production and/or T-cell proliferation by T-cells that have received a primary activation signal) are considered within the scope of the invention. For example, nucleic acid fragments that encode polypeptides or peptides of a B7-related factor that retain the ability of the polypeptides or peptides to bind CD28/CTLA-4 and/or CD28-/CTLA-4-related ligand(s) and deliver a modulatory (e.g., co-stimulatory

or inhibitory) signal to T-cells are within the scope of the invention. Generally, the nucleic acid molecule encoding a fragment of a B7-related factor will be selected from the coding sequence for the mature protein. However, in some instances it may be desirable to select all or part of a fragment or fragments from the coding region that includes the leader sequence.

In one embodiment of the present invention, a nucleic acid molecule corresponding to a fragment of a BSL2 nucleic acid sequence (e.g., **SEQ ID NO:**1, 2, 4, or 6, or complementary sequences) can be used as a probe for assaying a biological sample for the expression of one or more B7-related factors, or as a primer for DNA sequencing or PCR amplification. Preferably, such fragments are at least 8 contiguous nucleotides in length, more preferably at least 12 contiguous nucleotides in length, even more preferably at least 15 contiguous nucleotides in length, and even more preferably at least 20 contiguous nucleotides in length. Nucleic acid molecules within the scope of the invention may also contain linker sequences, modified restriction endonuclease sites, and other sequences useful for molecular cloning, expression, or purification of recombinant protein or fragments thereof. Nucleic acid molecules in accordance with the present invention may also be conjugated with radioisotopes, or chemiluminescent, fluorescent, or other labeling compounds (e.g., digoxigenin). In addition, the nucleic acid molecules of the present invention may be modified by nucleic acid modifying enzymes, for example, kinases or phosphatases. These and other modifications of nucleic acid molecules are well known in the art.

In addition, a nucleic acid molecule that encodes a B7-related factor, or a biologically active fragment thereof, can be ligated to a heterologous sequence to encode a fusion protein (also called a chimeric protein). For example, it may be useful to construct a nucleic acid encoding a fusion protein comprising a B7-related factor and the Fc domain of human IgG1 as described herein. In a preferred embodiment, the immunoglobulin sequences used in construction of the BSL2 immunofusion proteins of the present innovation are obtained from an IgG1 immunoglobulin heavy chain domain. The resulting BSL2-Ig, (e.g., **SEQ ID NO:**8, 10, or 12), and fusion

constructs can then be expressed in host cells, and used to prepare pharmaceutical compositions useful for immunomodulation (see below). Fusion proteins comprising B7-related polypeptides can also be used for the isolation and purification of B7-related polypeptides or antibodies (see below). In addition, fusion proteins can be used to identify cellular ligands or binding partners for BSL2 (see below).

In one aspect, polynucleotides encoding 1) a natural or heterologous signal sequence (ss); 2) a B7-related polypeptide (e.g., BSL2) that lacks a signal sequence; and 3) an Fc domain can be cloned serially to produce a fusion protein that can be depicted as ss-BSL2-Ig. Alternately, polynucleotides encoding 1) a natural or heterologous signal sequence (ss); 2) an Fc domain; and 3) a B7-related polypeptide (e.g., BSL2) that lacks a signal sequence can be cloned serially to produce a fusion protein that can be depicted as ss-Ig-ss-Ig-BSL2. Thus, B7-related polypeptide for this invention may be fused to the C-terminus or N-terminus of the Fc domain. In addition, the polynucleotide sequence may encode a proteolytic cleavage site positioned between the B7-related polypeptide and the Fc domain, which can be used to separate the B7-related polypeptide from the Fc domain. Notably, a major advantage of using IgG1 for protein fusions is that IgG1 immunofusions can be purified efficiently on immoblized protein A. However, other structural and functional properties may be considered when choosing the Ig fusion partner for a particular immunofusion construction.

B7-related nucleic acid expression vectors

Another aspect of the present invention pertains to expression vectors comprising a nucleic acid encoding at least one B7-related factor, as described herein, operably linked to at least one regulatory sequence. "Operably linked" is intended to mean that the nucleotide acid sequence is linked to a regulatory sequence in a manner that allows expression of the nucleotide sequence. Regulatory sequences are known in the art and are selected to direct expression of the desired protein in an appropriate host cell. Accordingly, the term regulatory sequence includes promoters, enhancers and other expression control elements (see D.V. Goeddel (1990) *Methods*

Enzymol. **185**:3-7). It should be understood that the design of the expression vector may depend on such factors as the choice of the host cell to be transfected and/or the type of polypeptide desired to be expressed.

Appropriate host cells for use with the present invention include bacteria, fungi, yeast, plant, insect, and animal cells, especially mammalian and human cells. Preferred replication and inheritance systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, CEN ARS, 2 μm ARS and the like. Several regulatory elements (e.g., promoters) have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Such regulatory regions, methods of isolation, manner of manipulation, etc. are known in the art. Non-limiting examples of bacterial promoters include the β-lactamase (penicillinase) promoter; lactose promoter; tryptophan (trp) promoter; araBAD (arabinose) operon promoter; lambda-derived P_1 promoter and N gene ribosome binding site; and the hybrid tac promoter derived from sequences of the trp and lac UV5 promoters. Non-limiting examples of yeast promoters include the 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactoepimerase promoter, and alcohol dehydrogenase (ADH1) promoter. Suitable promoters for mammalian cells include, without limitation, viral promoters, such as those from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV).

Eukaryotic cells may also require terminator sequences, polyadenylation sequences, and enhancer sequences that modulate gene expression. Sequences that cause amplification of the gene may also be desirable. These sequences are well known in the art. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or preprotein or proprotein sequences, may also be included. Such sequences are well described in the art.

Suitable expression vectors include, but are not limited to, pUC, pBluescript (Stratagene), pET (Novagen, Inc., Madison, WI), and pREP

(Invitrogen) plasmids. Vectors can contain one or more replication and inheritance systems for cloning or expression, one or more markers for selection in the host, e.g. antibiotic resistance, and one or more expression cassettes. The inserted coding sequences can be synthesized by standard methods, isolated from natural sources, or prepared as hybrids. Ligation of the coding sequences to transcriptional regulatory elements (e.g., promoters, enhancers, and/or insulators) and/or to other amino acid encoding sequences can be carried out using established methods.

In one embodiment, the expression vector comprises a nucleic acid encoding at least a portion of the BSL2 polypeptide. In another embodiment, the expression vector comprises a DNA sequence encoding the B7-related factor and a DNA sequence encoding another B7-related factor or a heterologous polypeptide or peptide. Such expression vectors can be used to transfect host cells to thereby produce polypeptides or peptides, including fusion proteins or peptides encoded by nucleic acid molecules as described below.

Isolation of B7-related polypeptides

Yet another aspect of the present invention pertains to methods of isolating B7-related polypeptides and related peptides. As used herein, the terms "protein" and "polypeptide" are synonymous. Peptides are defined as fragments or portions of proteins or polypeptides, preferably fragments or portions having the same or equivalent function or activity as the complete protein. Both naturally occurring and recombinant forms of the B7-related polypeptides or peptides may be used in assays and treatments according to the present invention. Methods for directly isolating and purifying polypeptides or peptides from natural sources such as cellular or extracellular lysates are well known in the art (see E.L.V. Harris and S. Angal, Eds. (1989) *Protein Purification Methods: A Practical Approach*, IRL Press, Oxford, England). Such methods include, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, high-performance liquid chromatography (HPLC), reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution, and combinations thereof.

Naturally occurring polypeptides can be purified from many possible sources, for example, plasma, body cells and tissues, or body fluids.

To produce recombinant B7-related polypeptides or peptides, DNA sequences encoding the B7-related polypeptides or peptides are cloned into a suitable vector for expression in intact host cells or in cell-free translation systems (see J. Sambrook et al., *supra*). Prokaryotic and eukaryotic vectors and host cells may be employed. The particular choice of a vector, host cell, or translation system is not critical to the practice of the invention. DNA sequences can be optimized, if desired, for more efficient expression in a given host organism. For example, codons can be altered to conform to the preferred codon usage in a given host cell or cell-free translation system using techniques routinely practiced in the art.

For some purposes, it may be preferable to produce peptides or polypeptides in a recombinant system wherein the peptides or polypeptides carry additional sequence tags to facilitate purification. Such markers include epitope tags and protein tags. Non-limiting examples of epitope tags include c-myc, haemagglutinin (HA), polyhistidine (6X-HIS; **SEQ ID NO:**15), GLU-GLU, and DYKDDDDK (FLAG®; **SEQ ID NO:**16) epitope tags. Epitope tags can be added to peptides by a number of established methods. DNA sequences of epitope tags can be inserted as oligonucleotides or through primers used in PCR amplification into or adjacent to a coding sequence of interest. As an alternative, a coding sequence of interest can be cloned into specific vectors that create fusions with epitope tags; for example, pRSET vectors (Invitrogen Corp., San Diego, CA). Non-limiting examples of protein tags include glutathione-S-transferase (GST), green fluorescent protein (GFP), and maltose binding protein (MBP). Protein tags are attached to peptides or polypeptides by several well-known methods. In one approach, the coding sequence of a polypeptide or peptide can be cloned into a vector that creates a fusion between the polypeptide or peptide and a protein tag of interest. Suitable vectors include, without limitation, the exemplary plasmids, pGEX (Amersham Pharmacia Biotech, Inc., Piscataway, NJ), pEGFP (CLONTECH Laboratories, Inc., Palo Alto, CA), and pMAL™ (New England

BioLabs, Inc., Beverly, MA). Following expression, the epitope or protein tagged polypeptide or peptide can be purified from a crude lysate of the translation system or host cell by chromatography on an appropriate solid-phase matrix. In some cases, it may be preferable to remove the epitope or protein tag (i.e., via protease cleavage) following purification.

Suitable cell-free expression systems for use in accordance with the present invention include rabbit reticulocyte lysate, wheat germ extract, canine pancreatic microsomal membranes, *E. coli* S30 extract, and coupled transcription/translation systems (Promega Corp., Madison, WI). These systems allow the expression of recombinant polypeptides or peptides upon the addition of cloning vectors, DNA fragments, or RNA sequences containing coding regions and appropriate promoter elements.

Host cells for recombinant cloning vectors include bacterial, archebacterial, fungal, plant, insect and animal cells, especially mammalian cells. Of particular interest are *E. coli*, *B. subtilis*, *S. aureus*, *S. cerevisiae*, *S. pombe*, *N. crassa*, SF9, C129, 293, NIH 3T3, CHO, COS, and HeLa cells. Such cells can be transformed, transfected, or transduced, as appropriate, by any suitable method including electroporation, $CaCl_2$-, LiCl-, LiAc/PEG-, spheroplasting-, Ca-Phosphate, DEAE-dextran, liposome-mediated DNA uptake, injection, microinjection, microprojectile bombardment, or other established methods.

In order to identify host cells that contain the expression vector, a gene that contains a selectable marker is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin, methotrexate, or ampicillin. Selectable markers can be introduced on the same plasmid as the gene of interest. Host cells containing the gene of interest are identified by drug selection, as cells that carry the drug-resistance marker survive in growth media containing the corresponding drug.

The surviving cells can be screened for production of recombinant B7-related polypeptides, or peptides or fusions thereof. In one embodiment, the recombinant polypeptides are secreted to the cell surface,

and can be identified by cell surface staining with ligands to the B cell antigens (e.g., CD28-Ig). In another embodiment, the recombinant polypeptides are retained in the cytoplasm of the host cells, and can be identified in cell extracts using anti-B7-related polypeptide antibodies. In yet another embodiment, soluble recombinant polypeptides are secreted into the growth media, and can be identified by screening the growth media with anti-B7-related polypeptide antibodies. A soluble, secreted recombinant B7-polypeptide includes the extracellular domain of the polypeptide, or any fragment thereof, that does not include the cytoplasmic and/or transmembrane regions. The cell-surface and cytoplasmic recombinant B7-related polypeptides can be isolated following cell lysis and extraction of cellular proteins, while the secreted recombinant B7-related polypeptides can be isolated from the cell growth media by standard techniques (see I.M. Rosenberg, Ed. (1996) *Protein Analysis and Purification: Benchtop Techniques*, Birkhauser, Boston, Cambridge, MA).

Antibody-based methods can used to purify natural or recombinantly produced B7-related polypeptides or peptides. Antibodies that recognize these polypeptides, or peptides derived therefrom, can be produced and isolated using methods known and practiced in the art (see below). B7-related polypeptides or peptides can then be purified from a crude lysate by chromatography on antibody-conjugated solid-phase matrices (see E. Harlow and D. Lane (1999) *Using Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY). Other purification methods known and used in the art may also be employed.

It is noted that transfected host cells that express B7-related factors (e.g., BSL2) or portions thereof on the surface of the cell are within the scope of this invention. For example, a tumor cell such as a sarcoma, melanoma, leukemia, lymphoma, carcinoma, or neuroblastoma can be transfected with an expression vector directing the expression of at least one B7-related factor on the surface of the tumor cell. Such transfected tumor cells can be used to treat tumor immunity as described in detail herein.

B7-related polypeptides

A further aspect of the present invention pertains to isolated B7-related polypeptides. The present invention encompasses the BSL2 polypeptides (e.g., **SEQ ID NO:**3, 5, or 7), and fragments and functional equivalents thereof. Such polypeptides can comprise at least 5, 12, 20, 30, 50, 90, 100, 170, 200, 210, 300, or 500 contiguous amino acid residues. Preferred are polypeptides that share moderate homology with BSL2 polypeptides (e.g., **SEQ ID NO:**3, 5, or 7). More preferred are polypeptides that share substantial homology with BSL2 (e.g., **SEQ ID NO:**3, 5, or 7).

The term "functional equivalent" is intended to include proteins which differ in amino acid sequence from a given B7-related polypeptide, such as sequence of BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7), but where such differences result in a modified protein which performs at least one characteristic function of the B7-related polypeptide (e.g., ligand-binding, antigenic, intra- or intercellular activity). For example, a functional equivalent of a BSL2 polypeptide may have a modification such as a substitution, addition or deletion of an amino acid residue which is not directly involved in the function of this polypeptide (i.e., the ability of these polypeptides to co-stimulate T-cell proliferation). In addition, non-naturally occurring analogs of B7-related polypeptides capable of binding CD28/CTLA-4 and/or CD28-/CTLA-4-related ligand(s) are considered functional equivalents. Various modifications of the B7-related polypeptides to produce functional equivalents of these polypeptides are described in detail herein.

As described herein below, the BSL4-4616811 (BSL2vcvc) polypeptide was determined to comprise a signal sequence from amino acid 1 to amino acid 28 of **SEQ ID NO:**3 (**Figure 1C**), according to the SPScan computer algorithm (Genetics Computer Group suite of programs). The site of signal sequence cleavage was confirmed by N-terminal sequencing of the BSL4-4616811 polypeptide. Based on this data, the mature BSL4-4616811 (BSL2vcvc) polypeptide sequence includes amino acid 29 to amino acid 534 of **SEQ ID NO:**3 (**Figure 1C**). As used herein a "mature sequence" is a polypeptide sequence that does not contain the signal sequence.

Accordingly, one embodiment of the present invention encompasses a polypeptide that lacks the signal sequence, but includes the remaining sequence of BSL2-4616811 (BSL2vcvc) polypeptide (i.e., the mature sequence of BSL2-4616811). Specifically, the invention encompasses a polypeptide comprising amino acids 29 through 534 of **SEQ ID NO:**3. The invention also encompasses a polynucleotide comprising nucleotides 85 through 1602 of **SEQ ID NO:**2, as well as a polypeptide comprising nucleotides 205 through 1722 of **SEQ ID NO:**1. Also encompassed are recombinant vectors comprising these polynucleotides, and host cells comprising these vectors.

Another embodiment of the present invention encompasses a polypeptide that lacks the signal sequence, but includes the remaining sequence of BSL2-L165-35b (BSL2v1c2) polypeptide, i.e., the mature sequence of BSL2-L165-35b. Specifically, the invention encompasses a polypeptide comprising amino acids 29 through 316 of **SEQ ID NO:**7. The invention also encompasses a polynucleotide comprising nucleotides 85 through 948 of **SEQ ID NO:**6. Also encompassed are recombinant vectors comprising these polynucleotides, and host cells comprising these vectors.

Yet another embodiment of the present invention encompasses a polypeptide that lacks the signal sequence, but includes the remaining sequence of BSL2-L165-21 (BSL2v2c2) polypeptide, i.e., the mature sequence of BSL2-L165-21. Specifically, the invention encompasses a polypeptide comprising amino acids 29 through 316 of **SEQ ID NO:**5 The invention also encompasses a polynucleotide comprising nucleotides 85 through 948 of **SEQ ID NO:**4. Also encompassed are recombinant vectors comprising these polynucleotides, and host cells comprising these vectors.

It is also possible that under certain conditions the BSL2 signal sequence cleavage site may vary. The invention therefore encompasses polypeptides that add or subtract 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 more contiguous amino acids from the N-terminus of the polypeptides described in the three proceeding paragraphs. Polynucleotides

encoding these polypeptides are also encompassed by the invention, as well as vectors and host cells comprising these polynucleotides.

It is possible to modify the structure of a B7-related polypeptide for such purposes as increasing solubility, enhancing therapeutic or prophylactic efficacy (reactivity), or stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). Such modified proteins are considered functional equivalents of the B7-related polypeptides as defined herein. Preferably, the B7-related polypeptides are modified so that they retain the ability to modulate (e.g., co-stimulate or inhibit) T-cell proliferation. Those residues shown to be essential to interact with the CD28/CTLA-4 or CD28-/CTLA-4-related ligands on T-cells can be modified by replacing the essential amino acid with another, preferably similar amino acid residue (a conservative substitution) whose presence is shown to enhance, diminish, but not eliminate, or not effect receptor interaction. In addition, those amino acid residues that are not essential for receptor interaction can be modified by being replaced by another amino acid whose incorporation may enhance, diminish, or not effect reactivity. For example, a B7-related polypeptide can be modified by substitution of cysteine residues with other amino acids, such as alanine, serine, threonine, leucine, or glutamic acid, to prevent dimerization via disulfide linkages. In addition, the amino acid side chains of a B7-related polypeptide of the invention can be chemically modified. Also, a B7-related polypeptide can be modified by cyclization of the amino acid sequence.

In order to enhance stability and/or reactivity, the B7-related polypeptides can be altered to incorporate one or more polymorphisms in the amino acid sequence. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified polypeptide. Furthermore, the B7-related polypeptides disclosed herein can be modified using polyethylene glycol (PEG) according to known methods (Wie et al., *supra*) to produce a protein conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other possible modifications include reduction/alkylation (Tarr (1986) *Methods of Protein Microcharacterization*, J. E. Silver, Ed., Humana Press, Clifton, NJ, pp. 155-

194); acylation (Tarr, *supra*); chemical coupling to an appropriate carrier (Mishell and Shiigi, Eds. (1980) *Selected Methods in Cellular Immunology*, W H Freeman, San Francisco, CA; U.S. Patent No. 4,939,239; or mild formalin treatment (Marsh (1971) *Int. Arch. of Allergy and Appl. Immunol.* **41**:199-215) of the B7-related polypeptide.

Modified polypeptides can have conservative changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More infrequently, a modified polypeptide can have non-conservative changes, e.g., substitution of a glycine with a tryptophan. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing biological or immunological activity can be found using computer programs well known in the art, for example, DNASTAR software (DNASTAR, Inc., Madison, WI)

As non-limiting examples, conservative substitutions in the B7-related amino acid sequence can be made in accordance with the following table.

Original Residue	Conservative Substitution(s)	Original Residue	Conservative Substitution(s)
Ala	Ser	Leu	Ile, Val
Arg	Lys	Lys	Arg, Gln, Glu
Asn	Gln, His	Met	Leu, Ile
Asp	Glu	Phe	Met, Leu, Tyr
Cys	Ser	Ser	Thr
Gln	Asn	Thr	Ser
Glu	Asp	Trp	Tyr
Gly	Pro	Tyr	Trp, Phe
His	Asn, Gln	Val	Ile, Leu
Ile	Leu, Val		

Substantial changes in function or immunogenicity can be made by selecting substitutions that are less conservative than those shown in the table, above. For example, non-conservative substitutions can be made which more significantly affect the structure of the polypeptide in the area of the alteration, for example, the alpha-helical, or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the

side chain. The substitutions which generally are expected to produce the greatest changes in the polypeptide's properties are those where 1) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl, or alanyl; 2) a cysteine or proline is substituted for (or by) any other residue; 3) a residue having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or 4) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) a residue that does not have a side chain, e.g., glycine.

Preferred polypeptide embodiments further include an isolated polypeptide comprising an amino acid sequence sharing at least 60, 70, 80, 85, 90, 95, 97, 98, 99, 99.5 or 100% identity with an amino acid sequence of BSL2 (e.g., **SEQ ID NO:**3, 5, or 7). This polypeptide sequence may be identical to the sequence of BSL2 (e.g., **SEQ ID NO:**3, 5, or 7), or may include up to a certain integer number of amino acid alterations as compared to the reference sequence

Percent sequence identity can be calculated using computer programs or direct sequence comparison. Preferred computer program methods to determine identity between two sequences include, but are not limited to, the GCG program package, FASTA, BLASTP, and TBLASTN (see, e.g., D.W. Mount, 2001, *Bioinformatics: Sequence and Genome Analysis*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). The BLASTP and TBLASTN programs are publicly available from NCBI and other sources. The well-known Smith Waterman algorithm may also be used to determine identity.

Exemplary parameters for amino acid sequence comparison include the following: 1) algorithm from Needleman and Wunsch (1970) *J. Mol. Biol.* **48**:443-453; 2) BLOSSUM62 comparison matrix from Hentikoff and Hentikoff (1992) *Proc. Natl. Acad. Sci. USA* **89**:10915-10919; 3) gap penalty = 12; and 4) gap length penalty = 4. A program useful with these parameters is publicly available as the "gap" program (Genetics Computer Group, Madison,

WI). The aforementioned parameters are the default parameters for polypeptide comparisons (with no penalty for end gaps).

Alternatively, polypeptide sequence identity can be calculated using the following equation: % identity = (the number of identical residues) / (alignment length in amino acid residues) * 100. For this calculation, alignment length includes internal gaps but does not include terminal gaps.

In accordance with the present invention, polypeptide sequences may be identical to the sequence of BSL2 (e.g., **SEQ ID NO:**3, 5, or 7), or may include up to a certain integer number of amino acid alterations. Polypeptide alterations are selected from the group consisting of at least one amino acid deletion, substitution, including conservative and non-conservative substitution, or insertion. Alterations may occur at the amino- or carboxy-terminal positions of the reference polypeptide sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. In specific embodiments, polypeptide variants may be encoded by BSL2 nucleic acids comprising single nucleotide polymorphisms and/or alternate splice variants. Polypeptides may also be modified by, for example, phosphorylation, sulfation, or acylation. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

In addition, the B7-related polypeptides of the invention can be fused to heterologous peptide or polypeptide sequences to create fusion proteins such as BSL2-4616811-Ig (e.g., **SEQ ID NO:**9), BSL2-L165-35b-Ig (e.g., **SEQ ID NO:**11), BSL2-L165-21-Ig (e.g., **SEQ ID NO:**13) as described in detail herein. In accordance with the experiments of the invention, the BSL2 sequence of BSL2-4616811-Ig (BSL2vcvc-Ig) polypeptide was determined to comprise a signal sequence from about amino acid 1 to about amino acid 28 of **SEQ ID NO:**9 (**Figure 4B**). The signal sequence cleavage site was determined using the SPScan computer algorithm (Genetics Computer Group suite of programs), and was confirmed by N-terminal sequencing. Based on

this data, the mature BSL2-4616811-Ig (BSL2vcvc-Ig) polypeptide sequence extends from amino acids 29 through 698 of **SEQ ID NO:9** (**Figure 4B**).

Accordingly, one embodiment of the present invention encompasses a BSL2-4616811-Ig (BSL2vcvc-Ig) polypeptide that includes amino acids 1 through 698 of **SEQ ID NO:9**. The invention also encompasses a BSL2-4616811-Ig (BSL2vcvc-Ig) polypeptide that lacks the initiating methionine, but includes amino acids 2 through 698 of **SEQ ID NO:9**. The invention further encompasses a polypeptide that lacks the signal sequence, but includes the remaining sequence of BSL2-4616811-Ig (BSL2vcvc-Ig) polypeptide, i.e., the mature sequence of BSL2-4616811-Ig. Specifically, the invention encompasses a polypeptide comprising amino acids 29 through 698 of **SEQ ID NO:9**. The invention also encompasses BSL2-4616811-Ig (BSL2vcvc-Ig) polynucleotides comprising nucleotides 1 through 2094, nucleotides 4 through 2094, or nucleotides 85 through 2094 of **SEQ ID NO:8**. Also encompassed are recombinant vectors comprising these polynucleotides, and host cells comprising these vectors.

Another embodiment of the present invention encompasses a BSL2-L165-35b-Ig (BSL2v1c2-Ig) polypeptide that includes amino acids 1 through 480 of **SEQ ID NO:11**. The invention also encompasses a BSL2-L165-35b-Ig (BSL2v1c2-Ig) polypeptide that lacks the initiating methionine, but includes amino acids 2 through 480 of **SEQ ID NO:11**. The invention further encompasses a polypeptide that lacks the signal sequence, but includes the remaining sequence of BSL2-L165-35b-Ig (BSL2v1c2-Ig) polypeptide, i.e., the mature sequence of BSL2-L165-35b-Ig. Specifically, the invention encompasses a polypeptide comprising amino acids 29 through 480 of **SEQ ID NO:11**. The invention also encompasses BSL2-L165-35b-Ig (BSL2v1c2-Ig) polynucleotides comprising nucleotides 1 through 1440, nucleotides 4 through 1440, or nucleotides 85 through 1440 of **SEQ ID NO:10**. Also encompassed are recombinant vectors comprising these polynucleotides, and host cells comprising these vectors.

Yet another embodiment of the present invention encompasses a BSL2-L165-21-Ig (BSL2v2c2-Ig) polypeptide that includes amino acids 1

through 480 of **SEQ ID NO:**13. The invention also encompasses a BSL2-L165-21-Ig (BSL2v2c2-Ig) polypeptide that lacks the initiating methionine, but includes amino acids 2 through 480 of **SEQ ID NO:**13. The invention further encompasses a polypeptide that lacks the signal sequence, but includes the remaining sequence of BSL2-L165-21-Ig (BSL2v2c2-Ig) polypeptide, i.e., the mature sequence of BSL2-L165-21-Ig. Specifically, the invention encompasses a BSL2-L165-21-Ig (BSL2v2c2-Ig) polypeptide comprising amino acids 29 through 480 of **SEQ ID NO:**13. The invention also encompasses BSL2-L165-21-Ig (BSL2v2c2-Ig) polynucleotides comprising nucleotides 1 through 1440, nucleotides 4 through 1440, or nucleotides 85 through 1440 of **SEQ ID NO:**12. Also encompassed are recombinant vectors comprising these polynucleotides, and host cells comprising these vectors.

It is also possible that under certain conditions the BSL2 signal sequence cleavage site may vary. The invention therefore encompasses polypeptides that add or subtract 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 more contiguous amino acids from the N-terminus of the polypeptides described in the three proceeding paragraphs. Polynucleotides encoding these polypeptides are also encompassed by the invention, as well as vectors and host cells comprising these polynucleotides.

The invention also relates to isolated, synthesized and/or recombinant portions or fragments of a BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7) as described herein. Polypeptide fragments (i.e., peptides) can be made which have full or partial function on their own, or which when mixed together (though fully, partially, or nonfunctional alone), spontaneously assemble with one or more other polypeptides to reconstitute a functional protein having at least one functional characteristic of a BSL2 protein of this invention. In addition, B7-related polypeptide fragments may comprise, for example, one or more domains of the polypeptide (e.g., the transmembrane or extracellular domain) disclosed herein.

The polypeptides of the present invention, including function-conservative variants, may be isolated from wild-type or mutant cells (e.g., human cells or cell lines), from heterologous organisms or cells (e.g., bacteria,

yeast, insect, plant, and mammalian cells), or from cell-free translation systems (e.g., wheat germ, microsomal membrane, or bacterial extracts) in which a protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins. The polypeptides can also, advantageously, be made by synthetic chemistry. Polypeptides may be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. Both the naturally occurring and recombinant forms of the polypeptides of the invention can advantageously be used to screen compounds for binding activity. The polypeptides of the invention also find use as therapeutic agents as well as antigenic components to prepare antibodies as described in detail herein.

Antibodies to B7-related polypeptides

Antibodies directed against the B7-related polypeptides of the present invention, e.g., BSL2 (e.g., **SEQ ID NO:**3, 5, or 7), or antigenic or immunogenic epitopes thereof, can be, for example, polyclonal or monoclonal antibodies. The present invention also includes chimeric, single chain, and humanized antibodies, as well as Fab, $F(ab')_2$, or Fv fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and antibody fragments.

Antibodies generated against the polypeptides or peptides corresponding to one or more of the B7-related sequences of the present invention can be obtained by direct injection of the polypeptides or peptides into an animal, or by administering the polypeptides or peptides to an animal, preferably a nonhuman animal. The antibodies so obtained will then bind to the polypeptides or peptides. In this manner, even a sequence encoding only a fragment of a polypeptide can be used to generate antibodies binding to the whole native polypeptide. Such antibodies can be used, for example, to isolate the polypeptide from tissue expressing that polypeptide.

For the preparation of monoclonal antibodies, any technique that provides antibodies produced by continuous cell line cultures can be used.

Examples include the hybridoma technique (Kohler and Milstein (1975) *Nature*, **256**:495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor et al. (1983) *Immunol. Today*, 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al. (1985) *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptide products of this invention. Also, transgenic mice may be used to express humanized antibodies to immunogenic polypeptide products of this invention.

The present invention encompasses polypeptides comprising, or alternatively, consisting of, an epitope of the polypeptide having an amino acid sequence of one or more of the BSL2 amino acid sequences as set forth in **Figures 1-6**. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of BSL2 of the invention. Typically, BSL2 epitopes comprise hydrophilic regions of the corresponding polypeptides (e.g., **SEQ ID NO:**3, 5, or 7). Hydrophilic regions can be determined by any method known in the art, for example, Kyte-Doolittle Hydrophilicity Plots (e.g., using the program bundle from Genetics Computer Group). In addition, the antigenic index can be determined directly using the Jameson-Wolf method (e.g., using the program bundle from Genetics Computer Group).

Non-limiting examples of BSL2-4616811 (BSL2vcvc) sequences which may be used as epitopes include sequences comprising amino acids 68 through 109; amino acids 148 through 186; amino acids 284 through 326; or amino acids 361 through 407 of **SEQ ID NO:**3. This invention also encompasses polynucleotides encoding these epitopes, and vectors and host cells comprising these polynucleotides. For example, such polynucleotides may comprise nucleotides 202 through 327; nucleotides 442 through 558; nucleotides 850 through 978; or nucleotides 1081 through 1221 of **SEQ ID NO:**2. Similarly, these polynucleotides may comprise nucleotides 322

through 447; nucleotides 562 through 678; nucleotides 970 through 1098; or nucleotides 1201 through 1341 of **SEQ ID NO:1**.

In preferred embodiments, the following immunogenic and/or antigenic epitopes are encompassed by the present invention: eptitopes comprising from about amino acid 68 to about amino acid 74, from about amino acid 75 to about amino acid 81, from about amino acid 82 to about amino acid 88, from about amino acid 89 to about amino acid 95, from about amino acid 96 to about amino acid 102, from about amino acid 103 to about amino acid 109, from about amino acid 148 to about amino acid 154, from about amino acid 155 to about amino acid 161, from about amino acid 162 to about amino acid 168, from about amino acid 169 to about amino acid 175, from about amino acid 176 to about amino acid 182, from about amino acid 183 to about amino acid 186, from about amino acid 284 to about amino acid 290, from about amino acid 291 to about amino acid 297, from about amino acid 298 to about amino acid 304, from about amino acid 305 to about amino acid 311, from about amino acid 312 to about amino acid 318, from about amino acid 319 to about amino acid 326, from about amino acid 361 to about amino acid 367, from about amino acid 368 to about amino acid 374, from about amino acid 375 to about amino acid 381, from about amino acid 387 to about amino acid 393, from about amino acid 394 to about amino acid 400, and/or from about amino acid 401 to about amino acid 407 of **SEQ ID NO:3**. In this context, the term "about" should be construed to mean 1, 2, 3, 4, or 5 more amino acids in either the N- or C-terminal direction of the above referenced epitopes. Polynucleotides encoding these polypeptides are also provided, as well as vectors and host cells comprising these polynucleotides.

The term "epitopes" as used herein, refers to portions of a polypeptide (e.g., peptides) having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope" as used herein, refers to a portion of a protein that elicits an antibody response in an animal, as determined by any method

known in the art, for example, by the methods for generating antibodies described *infra*. (See, for example, Geysen et al. (1983) *Proc. Natl. Acad. Sci. USA*, **81**:3998- 4002). The term "antigenic epitope" as used herein refers to a portion of a protein to which an antibody can immunospecifically bind to its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding, but does not necessarily exclude cross-reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic. Either the full-length protein or an antigenic peptide fragment can be used. Antibodies are preferably prepared from these regions or from discrete fragments in regions of the BSL2 nucleic acid and amino acid sequences comprising an epitope.

Moreover, antibodies can also be prepared from any region of the polypeptides and peptides of the B7-related sequences as described herein. A preferred fragment generates the production of an antibody that diminishes or completely prevents interaction with a binding partner. In addition, antibodies can be developed against an entire BSL2 polypeptide (e.g., **SEQ ID NO:**3, 5, or 7) or portions of the polypeptide, for example, a carboxy-terminal domain, an amino-terminal extracellular domain, an entire transmembrane domain, specific transmembrane segments, or any portions of these regions. Antibodies can also be developed against specific functional sites, such as the site of binding, or sites that are glycosylated, phosphorylated, myristylated, or amidated, for example. Also useful for antibody production are variable/constant (vc) domains of the B7-related polypeptides, e.g., the v1c2, v2c2, or v1c1v2c2 domains of BSL2 (see below). Polypeptide or peptide fragments that function as epitopes may be produced by any conventional means. (See, e.g., Houghten (1985) *Proc. Natl. Acad. Sci. USA*, **82**:5131-5135; and as described in U. S. Patent No. 4,631,211).

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and,

most preferably, between about 15 to about 30 contiguous amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 contiguous amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies that specifically bind the epitope. In addition, antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al. (1984) *Cell*, **37**:767-778; and Sutcliffe et al. (1983) *Science*, **219**:660-666). Such fragments as described herein are not to be construed, however, as encompassing any fragments that may be disclosed prior to the invention.

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., *supra*; Wilson et al., *supra*; Chow et al. (1985) *Proc. Natl. Acad. Sci. USA*, **82**:910-914; and Bittle et al. (1985) *J. Gen. Virol.*, **66**:2347-2354). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes.

B7-related polypeptides of the invention comprising one or more immunogenic epitopes that elicit an antibody response can be introduction together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse). Alternatively, if the polypeptide is of sufficient length (e.g., at least about 25 contiguous amino acids), the polypeptide can be presented without a carrier. However, immunogenic epitopes comprising as few as 5 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, *in vivo* immunization, *in vitro* immunization, and

phage display methods. See, e.g., Sutcliffe et al., *supra*; Wilson et al., *supra*; and Bittle et al., *supra*). If *in vivo* immunization is used, animals can be immunized with free peptide; however, the anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH), or tetanus toxoid (TT). For instance, peptides containing cysteine residues can be coupled to a carrier using a linker such as maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent, such as glutaraldehyde.

Epitope bearing peptides of the invention may also be synthesized as multiple antigen peptides (MAPs), first described by J.P. Tam et al. (1995) *Biomed. Pept, Proteins, Nucleic Acids*, 199, **1**(3):123-32; and Calvo, et al. (1993) *J. Immunol.*, **150**(4):1403-12), which are hereby incorporated by reference in their entirety herein. MAPs contain multiple copies of a specific peptide attached to a non-immunogenic lysine core. MAP peptides usually contain four or eight copies of the peptide, which are often referred to as MAP4 or MAP8 peptides. By way of non-limiting example, MAPs can be synthesized onto a lysine core matrix attached to a polyethylene glycol-polystyrene (PEG-PS) support. The peptide of interest is synthesized onto the lysine residues using 9-fluorenylmethoxycarbonyl (Fmoc) chemistry. For example, Applied Biosystems (Foster City, CA) offers commercially available MAP resins, such as, for example, the Fmoc Resin 4 Branch and the Fmoc Resin 8 Branch, which can be used to synthesize MAPs. Cleavage of MAPs from the resin is performed with standard trifloroacetic acid (TFA)-based cocktails known in the art. Purification of MAPs, except for desalting, is not generally necessary. MAP peptides can be used in immunizing vaccines which elicit antibodies that recognize both the MAP and the native protein from which the peptide was derived.

Epitope-bearing peptides of the invention can also be incorporated into a coat protein of a virus, which can then be used as an immunogen or a vaccine with which to immunize animals, including humans, in order stimulate the production of anti-epitope antibodies. For example, the

V3 loop of the gp120 glycoprotein of the human immunodeficiency virus type 1 (HIV-1) has been engineered to be expressed on the surface of rhinovirus. Immunization with rhinovirus displaying the V3 loop peptide yielded apparently effective mimics of the HIV-1 immunogens (as measured by their ability to be neutralized by anti-HIV-1 antibodies as well as by their ability to elicit the production of antibodies capable of neutralizing HIV-1 in cell culture). This techniques of using engineered viral particles as immunogens is described in more detail in Smith et al. (1997) *Behring Inst Mitt Feb*, **98**:229-39; Smith et al. (1998) *J. Virol.* **72**:651-659; and Zhang et al. (1999) *Biol. Chem.* **380**:365-74), which are hereby incorporated by reference herein in their entireties.

Epitope bearing polypeptides of the invention can be modified, for example, by the addition of amino acids at the amino- and/or carboxy-terminus of the peptide. Such modifications are performed, for example, to alter the conformation of the epitope bearing polypeptide such that the epitope will have a conformation more closely related to the structure of the epitope in the native protein. An example of a modified epitope-bearing polypeptide of the invention is a polypeptide in which one or more cysteine residues have been added to the polypeptide to allow for the formation of a disulfide bond between two cysteines, thus resulting in a stable loop structure of the epitope-bearing polypeptide under non-reducing conditions. Disulfide bonds can form between a cysteine residue added to the polypeptide and a cysteine residue of the naturally-occurring epitope, or between two cysteines which have both been added to the naturally-occurring epitope-bearing polypeptide.

In addition, it is possible to modify one or more amino acid residues of the naturally-occurring epitope-bearing polypeptide by substitution with cysteines to promote the formation of disulfide bonded loop structures. Cyclic thioether molecules of synthetic peptides can be routinely generated using techniques known in the art, e.g., as described in PCT publication WO 97/46251, incorporated in its entirety by reference herein. Other modifications of epitope-bearing polypeptides contemplated by this invention include biotinylation.

For the production of antibodies *in vivo*, host animals, such as rabbits, rats, mice, sheep, or goats, are immunized with either free or carrier-coupled peptides or MAP peptides, for example, by intraperitoneal and/or intradermal injection. Injection material is typically an emulsion containing about 100 μg of peptide or carrier protein and Freund's adjuvant, or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal can be increased by selection of anti-peptide antibodies, e.g., by adsorption of the peptide onto a solid support and elution of the selected antibodies according to methods well known in the art.

As one having skill in the art will appreciate, and as discussed above, the B7-related polypeptides of the present invention, which comprise an immunogenic or antigenic epitope, can be fused to other polypeptide sequences. For example, the polypeptides of the present invention can be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgD, or IgM), or portions thereof, e.g., CH1, CH2, CH3, or any combination thereof, and portions thereof, or with albumin (including, but not limited to, recombinant human albumin, or fragments or variants thereof (see, e.g., U.S. Patent No. 5,876,969; EP Patent No. 0 413 622; and U.S. Patent No. 5,766,883, incorporated by reference in their entirety herein), thereby resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life *in vivo*. This has been shown for chimeric proteins containing the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. See, e.g., Traunecker et al. (1988) *Nature* **331**:84-86).

Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner, such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG fusion proteins

that have a disulfide-linked dimeric structure due to the IgG portion disulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than are monomeric polypeptides, or fragments thereof, alone. See, e.g., Fountoulakis et al. (1995) *J. Biochem.* **270**:3958-3964).

Nucleic acids encoding epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system for the ready purification of non-denatured fusion proteins expressed in human cell lines has been described (Janknecht et al. (1991) *Proc. Natl. Acad. Sci. USA*, **88**:8972- 897). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag having six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto a Ni^{2+} nitriloacetic acid-agarose column and histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

Additional fusion proteins of the invention can be generated by employing the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling can be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al. (1997) *Curr. Opin. Biotechnol.* **8**:724-33; Harayama (1998) *Trends Biotechnol.* **16**(2):76-82; Hansson, et al. (1999) *J. Mol. Biol.* **287**:265-76; and Lorenzo and Blasco (1998) *Biotechniques*, **24**(2):308-313, the contents of each of which are hereby incorporated by reference in its entirety).

In an embodiment of the invention, alteration of polynucleotides corresponding to one or more of the B7-related polynucleotide sequences as set forth in **Figures 1-6**, and the polypeptides encoded by these polynucleotides, can be achieved by DNA shuffling. DNA shuffling involves

the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the polynucleotide sequence. In another embodiment, polynucleotides of the invention, or their encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion, or other methods, prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of this invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

Another aspect of the present invention relates to antibodies and T-cell antigen receptors (TCRs), which immunospecifically bind to a polypeptide, polypeptide fragment, or variant one or more of the BSL2 amino acid sequences as set forth in **Figures 1-6**, and/or an epitope thereof, of the present invention (as determined by immunoassays well known in the art for assaying specific antibody-antigen binding). The basic antibody structural unit of an antibody or immunoglobulin is known to comprise a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids; the variable region is primarily responsible for antigen recognition. The carboxy-terminal portion of each chain defines a constant region that is primarily responsible for immunoglobulin effector function. Immunoglobulin light chains, including human light chains, are of the kappa and lambda types. Immunoglobulin heavy chain isotypes include IgM, IgD, IgG, IgA, and IgE. (See, generally, W. Paul, Ed., (1989) *Fundamental Immunology*, Ch. 7, 2nd ed., Raven Press, N.Y., incorporated herein by reference in its entirety). The variable regions of each light/heavy chain pair form the antibody or immunoglobulin binding site. Thus, for example, an intact IgG antibody has two binding sites. Except in bifunctional or bispecific antibodies, the two binding sites are the same.

The chains of an immunoglobulin molecule exhibit the same general structure of relatively conserved framework regions (FR) joined by three hypervariable regions, also called complementarity determining regions or CDRs. The CDRs of the heavy and the light chains of each pair are aligned by the framework regions, thus enabling binding to a specific epitope. From N-terminus to C-terminus, both the light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4. The assignment of amino acids to each domain is in accordance with the definitions of Kabat Sequences of Proteins of Immunological Interest (National Institutes of Health, Bethesda, Md. (1987 and 1991)); Chothia and Lesk (1987) *J. Mol. Biol.* **196**:901-917; or Chothia et al. (1989) *Nature*, **342**:878-883.

A bispecific or bifunctional antibody is an artificial hybrid antibody having two different heavy/light chain pairs and two different binding sites. Bispecific antibodies can be produced by a variety of methods, including fusion of hybridomas or linking of Fab' fragments. (See, e.g., Songsivilai & Lachmann (1990) *Clin. Exp. Immunol.* **79**:315-321; Kostelny et al. (1992) *J. Immunol.* **148**:1547 1553). In addition, bispecific antibodies can be formed as "diabodies" (See, Holliger et al. (1993) *Proc. Natl. Acad. Sci. USA*, **90**:6444-6448), or "Janusins" (See, Traunecker et al. (1991) *EMBO J.*, **10**:3655-3659 and Traunecker et al. (1992) *Int. J. Cancer Suppl.* **7**:51-52).

Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), intracellularly made antibodies (i.e., intrabodies), and epitope-binding fragments of any of the above. The term "antibody", as used herein, refers to immunoglobulin molecules and immunologically active portions or fragments of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class or subclass (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) of

immunoglobulin molecule. In a preferred embodiment, the immunoglobulin is an IgG1 isotype. In another preferred embodiment, the immunoglobulin is an IgG2 isotype. In another preferred embodiment, the immunoglobulin is an IgG4 isotype.

Immunoglobulins may have both a heavy and a light chain. An array of IgG, IgE, IgM, IgD, IgA, and IgY heavy chains can be paired with a light chain of the kappa or lambda types. Most preferably, the antibodies of the present invention are human antigen-binding antibodies and antibody fragments and include, but are not limited to, Fab, Fab' F(ab') 2, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a V_L or V_H domain. Antigen-binding antibody fragments, including single-chain antibodies, can comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, and CH1, CH2, and CH3 domains. Also included in connection with the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, and CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are of human, murine (e.g., mouse and rat), donkey, sheep, rabbit, goat, guinea pig, camel, horse, or chicken origin. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described *infra* and, for example, in U.S. Patent No. 5,939,598.

The antibodies of the present invention can be monospecific, bispecific, trispecific, or of greater multispecificity. Multispecific antibodies can be specific for different epitopes of a polypeptide of the present invention, or can be specific for both a polypeptide of the present invention, and a heterologous epitope, such as a heterologous polypeptide or solid support material. (See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt et al. (1991) *J. Immunol.* **147**:60-69; U.S.

Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; and Kostelny et al. (1992) *J. Immunol.* **148**:1547-1553).

Antibodies of the present invention can be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention that they recognize or specifically bind. The epitope(s) or polypeptide portion(s) can be specified, e.g., by N-terminal and C-terminal positions, by size in contiguous amino acid residues, or as presented in the sequences defined in **Figures 1-6**, herein. Further included in accordance with the present invention are antibodies that bind to polypeptides encoded by polynucleotides that hybridize to a polynucleotide of the present invention under stringent, or moderately stringent, hybridization conditions as described herein.

The antibodies of the invention (including molecules comprising, or alternatively consisting of, antibody fragments or variants thereof) can bind immunospecifically to a polypeptide or polypeptide fragment or variant human B7-related polypeptide as set forth in **Figures 1-6** and/or monkey B7-related polypeptide.

By way of non-limiting example, an antibody can be considered to bind to a first antigen preferentially if it binds to the first antigen with a dissociation constant (Kd) that is less than the antibody's Kd for the second antigen. In another non-limiting embodiment, an antibody can be considered to bind to a first antigen preferentially if it binds to the first antigen with an affinity that is at least one order of magnitude less than the antibody's association constant (Ka) for the second antigen. In another non-limiting embodiment, an antibody can be considered to bind to a first antigen preferentially if it binds to the first antigen with an affinity that is at least two orders of magnitude less than the antibody's Kd for the second antigen.

In another nonlimiting embodiment, an antibody may be considered to bind to a first antigen preferentially if it binds to the first antigen with an off rate (Koff) that is less than the antibody's Koff for the second antigen. In another nonlimiting embodiment, an antibody can be considered to bind to a first antigen preferentially if it binds to the first antigen with an

affinity that is at least one order of magnitude less than the antibody's Koff for the second antigen. In another nonlimiting embodiment, an antibody can be considered to bind to a first antigen preferentially if it binds to the first antigen with an affinity that is at least two orders of magnitude less than the antibody's Koff for the second antigen.

Antibodies of the present invention can also be described or specified in terms of their binding affinity to a B7-related polypeptide of the present invention. Preferred binding affinities include those with a dissociation constant or Kd of less than 5×10^{-2} M, 1×10^{-2} M, 5×10^{-3} M, 1×10^{-3} M, 5×10^{-4} M, or 1×10^{-4} M. More preferred binding affinities include those with a dissociation constant or Kd less than 5×10^{-5} M, 1×10^{-5} M, 5×10^{-6} M, 1×10^{-6} M, 5×10^{-7} M, 1×10^{-7} M, 5×10^{-8} M, or 1×10^{-8} M. Even more preferred antibody binding affinities include those with a dissociation constant or Kd of less than 5×10^{-9} M, 1×10^{-9} M, 5×10^{-10} M, 1×10^{-10} M, 5×10^{-11} M, 1×10^{-11} M, 5×10^{-12} M, 1×10^{-12} M, 5×10^{-13} M, 1×10^{-13} M, 5×10^{-14} M, 1×10^{-14} M, 5×10^{-15} M, or 1×10^{-15} M.

In specific embodiments, antibodies of the invention bind to B7-related polypeptides of the invention, or fragments, or variants thereof, with an off rate (Koff) of less than or equal to about 5×10^{-2} sec^{-1}, 1×10^{-2} sec^{-1}, 5×10^{-3} sec^{-1}, or 1×10^{-3} sec^{-1}. More preferably, antibodies of the invention bind to B7-related polypeptides of the invention or fragments or variants thereof with an off rate (Koff) of less than or equal to about 5×10^{-4} sec^{-1}, 1×10^{-4} sec^{-1}, 5×10^{-5} sec^{-1}, 1×10^{-5} sec^{-1}, 5×10^{-6} sec^{-1}, 1×10^{-6} sec^{-1}, 5×10^{-7} sec^{-1}, or 1×10^{-7} sec^{-1}.

In other embodiments, antibodies of the invention bind to B7-related polypeptides of the invention or fragments or variants thereof with an on rate (Kon) of greater than or equal to 1×10^{3} M^{-1} sec^{-1}, 5×10^{3} M^{-1} sec^{-1}, 1×10^{4} M^{-1} sec^{-1}, or 5×10^{4} M^{-1} sec^{-1}. More preferably, antibodies of the invention bind to B7-related polypeptides of the invention or fragments or variants thereof with an on rate greater than or equal to 1×10^{5} M^{-1} sec^{-1}, 5×10^{5} M^{-1} sec^{-1}, 1×10^{6} M^{-1} sec^{-1}, 5×10^{6} M^{-1} sec^{-1}, or 1×10^{7} M^{-1} sec^{-1}.

The present invention also provides antibodies that competitively inhibit the binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays as described herein. In preferred embodiments, the antibody competitively inhibits binding to an epitope by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Antibodies of the present invention may act as agonists or antagonists of the B7-related polypeptides of the present invention. For example, the present invention includes antibodies that disrupt the intra-cellular or inter-cellular activity, or interactions, of the polypeptides of the invention either partially or fully. The invention includes BSL2-specific antibodies and antibody specific for the corresponding BSL-binding partner complexes. The invention also includes BSL2-specific antibodies which do not prevent interaction with a cognate binding partner (e.g., ligand), but do prevent activation. Activation (i.e., signaling) can be determined by techniques described herein or as otherwise known in the art. In specific embodiments, antibodies are provided that inhibit BSL2 binding activity or activation activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in the absence of the antibody.

In another embodiment of the present invention, antibodies that immunospecifically bind to a B7-related polypeptide of the invention or a fragment or variant thereof, comprise a polypeptide having the amino acid sequence of any one of the heavy chains expressed by an anti-BSL2 antibody-expressing cell line of the invention, and/or any one of the light chains expressed by an anti-BSL2 antibody-expressing cell line of the invention. In another embodiment of the present invention, antibodies that immunospecifically bind to a B7-related polypeptide of the invention or a fragment or variant thereof, comprise a polypeptide having the amino acid sequence of any one of the V_H domains of a heavy chain expressed by an anti-BSL2 antibody-expressing cell line, and/or any one of the V_L domains of a

light chain expressed by an anti-BSL2 antibody-expressing cell line. In preferred embodiments, antibodies of the present invention comprise the amino acid sequence of a V_H domain and V_L domain expressed by a single anti-BSL2 antibody-expressing cell line. In alternative embodiments, antibodies of the present invention comprise the amino acid sequence of a V_H domain and a V_L domain expressed by two different anti-BSL2 antibody-expressing cell lines.

Molecules comprising, or alternatively consisting of, antibody fragments or variants of the V_H and/or V_L domains expressed by an anti-BSL2 antibody-expressing cell line that immunospecifically bind to a B7-related polypeptide of the invention are also encompassed by the invention, as are nucleic acid molecules encoding these V_H and V_L domains, molecules, fragments and/or variants.

The present invention also provides antibodies that immunospecificially bind to a polypeptide, or polypeptide fragment or variant of a B7-related polypeptide such as BSL2 (e.g., **SEQ ID NO:**3, 5, or 7), wherein said antibodies comprise, or alternatively consist of, a polypeptide having an amino acid sequence of any one, two, three, or more of the V_H CDRs contained in a heavy chain expressed by one or more anti-BSL2 antibody expressing cell lines. In particular, the invention provides antibodies that immunospecifically bind to a B7-related polypeptide of the invention, comprising, or alternatively consisting of, a polypeptide having the amino acid sequence of a V_H CDR1 contained in a heavy chain expressed by one or more anti-BSL2 antibody expressing cell lines. In another embodiment, antibodies that immunospecifically bind to a B7-related polypeptide of the invention, comprise, or alternatively consist of, a polypeptide having the amino acid sequence of a V_H CDR2 contained in a heavy chain expressed by one or more anti-BSL2 antibody expressing cell lines. In a preferred embodiment, antibodies that immunospecifically bind to a B7-related polypeptide of the invention, comprise, or alternatively consist of, a polypeptide having the amino acid sequence of a V_H CDR3 contained in a heavy chain expressed by one or more anti-BSL2 antibody expressing cell line of the invention. Molecules

comprising, or alternatively consisting of, these antibodies, or antibody fragments or variants thereof, that immunospecifically bind to a B7-related polypeptide (e.g., BSL2) or a polypeptide fragment or variant thereof are also encompassed by the invention, as are nucleic acid molecules encoding these antibodies, molecules, fragments and/or variants.

The present invention also provides antibodies that immunospecificially bind to a polypeptide, or polypeptide fragment or variant of a B7-related polypeptide disclosed herein, wherein said antibodies comprise, or alternatively consist of, a polypeptide having an amino acid sequence of any one, two, three, or more of the V_L CDRs contained in a heavy chain expressed by one or more anti-BSL2 antibody expressing cell lines of the invention. In particular, the invention provides antibodies that immunospecifically bind to a B7-related polypeptide disclosed herein, comprising, or alternatively consisting of, a polypeptide having the amino acid sequence of a V_L CDR1 contained in a heavy chain expressed by one or more anti-BSL2 antibody-expressing cell lines of the invention. In another embodiment, antibodies that immunospecifically bind to a B7-related polypeptide of the invention, comprise, or alternatively consist of, a polypeptide having the amino acid sequence of a V_L CDR2 contained in a heavy chain expressed by one or more anti-BSL2 antibody-expressing cell lines of the invention. In a preferred embodiment, antibodies that immunospecifically bind to a B7-related polypeptide of the invention, comprise, or alternatively consist of a polypeptide having the amino acid sequence of a V_L CDR3 contained in a heavy chain expressed by one or more anti-BSL2 antibody-expressing cell lines of the invention. Molecules comprising, or alternatively consisting of, these antibodies, or antibody fragments or variants thereof, that immunospecifically bind to a B7-related polypeptide such as BSL2 (e.g., **SEQ ID NO:**3, 5, or 7), or a polypeptide fragment or variant thereof are also encompassed by the invention, as are nucleic acid molecules encoding these antibodies, molecules, fragments and/or variants.

The present invention also provides antibodies (including molecules comprising, or alternatively consisting of, antibody fragments or variants) that immunospecifically bind to a B7-related polypeptide, or polypeptide fragment or variant disclosed herein, wherein the antibodies comprise, or alternatively consist of, one, two, three, or more V_H CDRs, and one, two, three or more V_L CDRs, as contained in a heavy chain or light chain expressed by one or more anti-BSL2 antibody-expressing cell lines of the invention. In particular, the invention provides antibodies that immunospecifically bind to a polypeptide or polypeptide fragment or variant of a B7-related polypeptide disclosed herein, wherein the antibodies comprise, or alternatively consist of, a V_H CDR1 and a V_L CDR1, a V_H CDR1 and a V_L CDR2, a V_H CDR1 and a V_L CDR3, a V_H CDR2 and a V_L CDR1, VH CDR2 and V_L CDR2, a V_H CDR2 and a V_L CDR3, a V_H CDR3 and a V_H CDR1, a V_H CDR3 and a V_L CDR2, a V_H CDR3 and a V_L CDR3, or any combination thereof, of the V_H CDRs and V_L CDRs contained in a heavy chain or light chain immunoglobulin molecule expressed by one or more anti-BSL2 antibody-expressing cell lines of the invention. In a preferred embodiment, one or more of these combinations are from a single anti-BSL2 antibody-expressing cell line of the invention. Molecules comprising, or alternatively consisting of, fragments or variants of these antibodies that immunospecifically bind to a B7-related polypeptide such as BSL2 (e.g., **SEQ ID NO:**3, 5, or 7) are also encompassed by the invention, as are nucleic acid molecules encoding these antibodies, molecules, fragments or variants.

The present invention also provides nucleic acid molecules, generally isolated, encoding an antibody of the invention (including molecules comprising, or alternatively consisting of, antibody fragments or variants thereof). In a specific embodiment, a nucleic acid molecule of the invention encodes an antibody (including molecules comprising, or alternatively consisting of, antibody fragments or variants thereof), comprising, or alternatively consisting of, a V_H domain having an amino acid sequence of any one of the V_H domains of a heavy chain expressed by an anti-BSL2 antibody-expressing cell line of the invention and a V_L domain having an

amino acid sequence of a light chain expressed by an anti-BSL2 antibody-expressing cell line of the invention. In another embodiment, a nucleic acid molecule of the invention encodes an antibody (including molecules comprising, or alternatively consisting of, antibody fragments or variants thereof), comprising, or alternatively consisting of, a V_H domain having an amino acid sequence of any one of the V_H domains of a heavy chain expressed by an anti-BSL2 antibody-expressing cell line of the invention, or a V_L domain having an amino acid sequence of a light chain expressed by an anti-BSL2 antibody-expressing cell line of the invention.

The present invention also provides antibodies that comprise, or alternatively consist of, variants (including derivatives) of the antibody molecules (e.g., the V_H domains and/or V_L domains) described herein, which antibodies immunospecifically bind to a B7-related polypeptide or fragment or variant thereof, as disclosed herein.

Standard techniques known to those of skill in the art can be used to introduce mutations in the nucleotide sequence encoding a molecule of the invention, including, for example, site-directed mutagenesis and PCR-mediated mutagenesis which result in amino acid substitutions. Preferably the molecules are immunoglobulin molecules. Also, preferably, the variants (including derivatives) encode less than 50 amino acid substitutions, less than 40 amino acid substitutions, less than 30 amino acid substitutions, less than 25 amino acid substitutions, less than 20 amino acid substitutions, less than 15 amino acid substitutions, less than 10 amino acid substitutions, less than 5 amino acid substitutions, less than 4 amino acid substitutions, less than 3 amino acid substitutions, or less than 2 amino acid substitutions, relative to the reference V_H domain, V_H CDR1, V_H CDR2, V_H CDR3, V_L domain, V_L CDR1, V_L CDR2, or V_L CDR3.

A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a side chain with a similar charge. Families of amino acid residues having side chains with similar charges have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side

chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis. The resultant mutants can be screened for biological activity to identify mutants that retain activity.

For example, it is possible to introduce mutations only in framework regions or only in CDR regions of an antibody molecule. Introduced mutations can be silent or neutral missense mutations, i.e., have no, or little, effect on an antibody's ability to bind antigen. These types of mutations can be useful to optimize codon usage, or to improve hybridoma antibody production. Alternatively, non-neutral missense mutations can alter an antibody's ability to bind antigen. The location of most silent and neutral missense mutations is likely to be in the framework regions, while the location of most non-neutral missense mutations is likely to be in the CDRs, although this is not an absolute requirement. One of skill in the art is able to design and test mutant molecules with desired properties, such as no alteration in antigen binding activity or alteration in binding activity (e.g., improvements in antigen binding activity or change in antibody specificity). Following mutagenesis, the encoded protein may routinely be expressed and the functional and/or biological activity of the encoded protein can be determined using techniques described herein or by routinely modifying techniques known and practiced in the art.

In a specific embodiment, an antibody of the invention (including a molecule comprising, or alternatively consisting of, an antibody fragment or variant thereof), that immunospecifically binds to B7-related polypeptides or fragments or variants disclosed herein, comprises, or alternatively consists of, an amino acid sequence encoded by a nucleotide sequence that hybridizes to a nucleotide sequence that is complementary to that encoding one of the V_H

or V_L domains expressed by one or more anti-BSL2 antibody-expressing cell lines of the invention, preferably under stringent conditions, e.g., hybridization to filter-bound DNA in 6 X sodium chloride/sodium citrate (SSC) at about 45°C followed by one or more washes in 0.2 X SSC/0.1% SDS at about 50-65°C, preferably under highly stringent conditions, e.g., hybridization to filter-bound nucleic acid in 6 X SSC at about 45°C followed by one or more washes in 0.1 X SSC/0.2% SDS at about 68°C, or under other stringent hybridization conditions which are known to those of skill in the art (see, for example, F.M. Ausubel et al., eds. (1989) *Current Protocols in Molecular Biology*, Vol. I, Green Publishing Associates, Inc. and John Wiley & Sons, Inc., New York at pages 6.3.1-6.3.6 and 2.10.3). Nucleic acid molecules encoding these antibodies are also encompassed by the invention.

It is well known within the art that polypeptides, or fragments or variants thereof, with similar amino acid sequences often have similar structure and many of the same biological activities. Thus, in one embodiment, an antibody (including a molecule comprising, or alternatively consisting of, an antibody fragment or variant thereof), that immunospecifically binds to a B7-related polypeptide or fragments or variants of a B7-related polypeptide disclosed herein, comprises, or alternatively consists of, a V_H domain having an amino acid sequence that is at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identical to the amino acid sequence of a V_H domain of a heavy chain expressed by an anti-BSL2 antibody-expressing cell line of the invention.

In another embodiment, an antibody (including a molecule comprising, or alternatively consisting of, an antibody fragment or variant thereof), that immunospecifically binds to a B7-related polypeptide or fragments or variants of a B7-related polypeptide disclosed herein, comprises, or alternatively consists of, a V_L domain having an amino acid sequence that is at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at

least 90%, at least 95%, or at least 99% identical to the amino acid sequence of a V_L domain of a light chain expressed by an anti-BSL2 antibody-expressing cell line of the invention.

The present invention also provides antibodies (including molecules comprising, or alternatively consisting of, antibody fragments or variants thereof), that down-regulate the cell-surface expression of a B7-related polypeptide of the invention, as determined by any method known in the art such as, for example, FACS analysis or immunofluorescence assays. By way of a non-limiting hypothesis, such down-regulation may be the result of antibody induced internalization of B7-related polypeptide of the invention. Such antibodies can comprise, or alternatively consist of, a portion (e.g., V_H CDR1, V_H CDR2, V_H CDR3, V_L CDR1, V_L CDR2, or V_L CDR3) of a V_H or V_L domain having an amino acid sequence of an antibody of the invention, or a fragment or variant thereof.

In another embodiment, an antibody that down-regulates the cell-surface expression of a B7-related polypeptide of the invention comprises, or alternatively consists of, a polypeptide having the amino acid sequence of a V_H domain of an antibody of the invention, or a fragment or variant thereof and a V_L domain of an antibody of the invention, or a fragment or variant thereof. In another embodiment, an antibody that down-regulates the cell-surface expression of a B7-related polypeptide of the invention comprises, or alternatively consists of, a polypeptide having the amino acid sequence of a V_H domain and a V_L domain from a single antibody (or scFv or Fab fragment) of the invention, or fragments or variants thereof. In another embodiment, an antibody that down-regulates the cell-surface expression of a B7-related polypeptide of the invention comprises, or alternatively consists of, a polypeptide having the amino acid sequence of a V_H domain of an antibody of the invention, or a fragment or variant thereof. In another embodiment, an antibody that down-regulates the cell-surface expression of a B7-related polypeptide of the invention comprises, or alternatively consists of, a polypeptide having the amino acid sequence of a V_L domain of an antibody of the invention, or a fragment or variant thereof.

In a preferred embodiment, an antibody that down-regulates the cell-surface expression of a B7-related polypeptide of the invention comprises, or alternatively consists of, a polypeptide having the amino acid sequence of a V_H CDR3 of an antibody of the invention, or a fragment or variant thereof. In another preferred embodiment, an antibody that down-regulates the cell-surface expression of a B7-related polypeptide of the invention comprises, or alternatively consists of, a polypeptide having the amino acid sequence of a V_L CDR3 of an antibody of the invention, or a fragment or variant thereof. Nucleic acid molecules encoding these antibodies are also encompassed by the invention.

In another preferred embodiment, an antibody that enhances the activity of a B7-related polypeptide, or a fragment or variant disclosed herein, comprises, or alternatively consists of, a polypeptide having the amino acid sequence of a V_L CDR3 of an antibody of the invention, or a fragment or variant thereof. Nucleic acid molecules encoding these antibodies are also encompassed by the invention.

As nonlimiting examples, antibodies of the present invention can be used to purify, detect, and target the polypeptides of the present invention, including both *in vitro* and *in vivo* diagnostic, detection, screening, and/or therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the B7-related polypeptides of the present invention in biological samples. (See, e.g., Harlow et al. (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, 2nd Ed., which is incorporated by reference herein in its entirety).

By way of another nonlimiting example, antibodies of the invention can be administered to individuals as a form of passive immunization. Alternatively, antibodies of the present invention can be used for epitope mapping to identify the epitope(s) that are bound by the antibody. Epitopes identified in this way can, in turn, for example, be used as vaccine candidates, i.e., to immunize an individual to elicit antibodies against the

naturally-occurring forms of one or more B7-related polypeptides of the invention.

As discussed in more detail below, the antibodies of the present invention can be used either alone or in combination with other compositions. The antibodies can further be recombinantly fused to a heterologous polypeptide at the N-or C-terminus, or chemically conjugated (including covalent and non-covalent conjugations) to polypeptides or other compositions. For example, antibodies of the present invention can be recombinantly fused or conjugated to molecules that are useful as labels in detection assays and to effector molecules such as heterologous polypeptides, drugs, radionucleotides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995 and EP 396, 387.

The antibodies of the invention include derivatives that are modified, i.e., by the covalent attachment of any type of molecule to the antibody. For example, without limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to, specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative can contain one or more non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method known in the art. Polyclonal antibodies directed against an antigen or immunogen of interest can be produced by various procedures well known in the art. For example, a B7-related polypeptide or peptide of the invention can be administered to various host animals as elucidated above to induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species; adjuvants include, but are not

limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art, including the use of hybridoma, recombinant and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques as known and practiced in the art (as taught, for example, in Harlow et al. (1988) *Antibodies: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 2nd Ed.; and Hammerling, et al., (1981) *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, NY, pages 563-681, the contents of which are incorporated herein by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art. In a nonlimiting example, mice can be immunized with a polypeptide or peptide of the invention, or with a cell expressing the polypeptide or peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the sera of immunized mice, the spleen is harvested and splenocytes are isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP2/0 or P3X63-AG8.653 available from the ATCC. Hybridomas are selected and cloned by limiting dilution techniques. The hybridoma clones are then assayed by methods known in the art to determine and select those cells that secrete antibodies capable of binding to a polypeptide of the invention.

Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention encompasses methods of generating monoclonal antibodies, as well as the antibodies produced by these methods, comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with a B7-related polypeptide or peptide antigen of the invention with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody that binds to a polypeptide of the invention such as BSL2 (e.g., **SEQ ID NO:**3, 5, or 7).

Another well known method for producing both polyclonal and monoclonal human B cell lines is transformation using Epstein Barr Virus (EBV). Protocols for generating EBV-transformed B cell lines are commonly known in the art (see, for example, the protocol outlined in Chapter 7.22 of Coligan et al., Eds., (1994) *Current Protocols in Immunology*, John Wiley & Sons, NY, which is hereby incorporated by reference herein in its entirety). The source of B cells for transformation is commonly human peripheral blood, but B cells for transformation can also be obtained from other sources including, but not limited to, lymph node, tonsil, spleen, tumor tissue, and infected tissues. Tissues are generally prepared as single cell suspensions prior to EBV transformation. In addition, T-cells that may be present in the B cell samples can be either physically removed or inactivated (e.g., by treatment with cyclosporin A). The removal of T-cells is often advantageous, because T-cells from individuals seropositive for anti-EBV antibodies can suppress B cell immortalization by EBV. In general, a sample containing human B cells is inoculated with EBV and cultured for 3-4 weeks. A typical source of EBV is the culture supernatant of the B95-8 cell line (ATCC; VR-1492). Physical signs of EBV transformation can generally be seen toward the end of the 3-4 week culture period.

By phase-contrast microscopy, transformed cells appear large, clear and "hairy"; they tend to aggregate in tight clusters of cells. Initially, EBV

lines are generally polyclonal. However, over prolonged periods of cell culture, EBV lines can become monoclonal as a result of the selective outgrowth of particular B cell clones. Alternatively, polyclonal EBV transformed lines can be subcloned (e.g., by limiting dilution) or fused with a suitable fusion partner and plated at limiting dilution to obtain monoclonal B cell lines. Suitable fusion partners for EBV transformed cell lines include mouse myeloma cell lines (e.g., SP2/0, X63-Ag8.653), heteromyeloma cell lines (human x mouse ; e.g., SPAM-8, SBC-H20, and CB-F7), and human cell lines (e.g., GM 1500, SKO-007, RPMI 8226, and KR-4). Thus, the present invention also includes a method of generating polyclonal or monoclonal human antibodies against polypeptides of the invention or fragments thereof, comprising EBV-transformation of human B cells.

Antibody fragments that recognize specific epitopes can be generated by known techniques. For example, Fab and F(ab')2 fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F (ab') 2 fragments). F(ab')2 fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

Antibodies encompassed by the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles that carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds to the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured onto a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used

to make the antibodies of the present invention include those disclosed in Brinkman et al. (1995) *J. Immunol. Methods*, **182**:41-50; Ames et al. (1995) *J. Immunol. Methods*, **184**:177-186; Kettleborough et al. (1994) *Eur. J. Immunol.* **24**:952-958; Persic et al. (1997) *Gene*, **187**:9-18; Burton et al. (1994) *Advances in Immunology*, **57**:191-280; PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108, each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')2 fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al. (1992) *BioTechniques*, **12**(6):864-869; Sawai et al. (1995) *AJRI*, **34**:2634; and Better et al. (1988) *Science*, **240**:1041-1043, which are hereby incorporated by reference herein in their entireties.

Examples of techniques that can be used to produce single-chain Fvs and antibodies include those described in U.S. Patent Nos. 4,946,778 and 5,258,498; Huston et al. (1991) *Methods Enzymol.*, **203**:46-88; Shu et al. (1993) *Proc. Natl. Acad. Sci. USA*, **90**:7995-7999; and Skerra et al. (1988) *Science*, **240**:1038-1040. For some uses, including the *in vivo* use of antibodies in humans and in *in vitro* detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region.

Methods for producing chimeric antibodies are known in the art. (See, e.g., Morrison (1985) *Science*, **229**:1202; Oi et al. (1986) *BioTechniques*, 4:214; Gillies et al. (1989) *J. Immunol. Methods*, **125**:191-202; and U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entirety).

Humanized antibodies are antibody molecules from non-human species antibody that bind to the desired antigen and have one or more complementarity determining regions (CDRs) from the nonhuman species and framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions are substituted with the corresponding residues from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding, and by sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Patent No. 5,585,089; and Riechmann et al. (1988) *Nature*, **332**:323, which are incorporated herein by reference in their entireties). Antibodies can be humanized using a variety of techniques known in the art, including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos. 5,225,539; 5,530,101; and 5,585,089); veneering or resurfacing (EP 592,106; EP 519,596; Padlan (1991) *Molecular Immunology*, **28**:489-498; Studnicka et al. (1994) *Protein Engineering*, **7**(6):805-814; Roguska et al. (1994) *Proc. Natl. Acad. Sci. USA*, **91**:969-973; and chain shuffling (U.S. Patent No. 5,565,332).

Completely human antibodies can be made by a variety of methods known in the art, including the phage display methods described above, using antibody libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients, so as to avoid or alleviate immune reaction to foreign protein. Human antibodies can be made by a variety of methods known in the art, including the phage display methods described above, using antibody libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes can be introduced randomly, or by homologous recombination, into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells, in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes can be rendered nonfunctional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the J_H region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring that express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention.

Monoclonal antibodies directed against the antigen can be obtained from the immunized transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation.

Thus, using such a technique, it is possible to produce useful human IgG, IgA, IgM and IgE antibodies. For an overview of the technology for producing human antibodies, see Lonberg and Huszar (1995) *Intl. Rev. Immunol.* **13**:65-93. For a detailed discussion of the technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent No. 0 598 877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; 5,939,598; 6,075,181; and 6,114,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Fremont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed against a selected antigen using technology similar to the above described technologies.

Completely human antibodies that recognize a selected epitope can be generated using a technique referred to as "guided selection". In this approach, a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers et al. (1988) *BioTechnology*, **12**:899-903).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotypic antibodies that "mimic" B7-related polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan and Bona (1989) *FASEB J.* **7**(5):437-444 and Nissinoff (1991) *J. Immunol.* **147**(8):2429-2438). For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" one or more of the BSL-1, BSL2, or BSL2 polypeptide domains and, as a consequence, bind to and neutralize the polypeptide and/or its binding partner, e.g., in therapeutic regimens. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used to neutralize polypeptide activity. For example, such anti-idiotypic antibodies

can be used to bind a polypeptide of the invention and/or to bind its , and thereby activate or block its biological activity.

Intrabodies are antibodies, often scFvs, that are expressed from a recombinant nucleic acid molecule and are engineered to be retained intracellularly (e.g., retained in the cytoplasm, endoplasmic reticulum, or periplasm of the host cells). Intrabodies can be used, for example, to ablate the function of a protein to which the intrabody binds. The expression of intrabodies can also be regulated through the use of inducible promoters in the nucleic acid expression vector comprising nucleic acid encoding the intrabody. Intrabodies of the invention can be produced using methods known in the art, such as those disclosed and reviewed in Chen et al. (1994) *Hum. Gene Ther.* **5**:595-601; W.A. Marasco (1997) *Gene Ther.* **4**:11-15; Rondon and Marasco (1997) *Annu. Rev. Microbiol.* **51**:257-283; Proba et al. (1998) *J. Mol. Biol.* **275**:245-253; Cohen et al. (1998) *Oncogene*, **17**:2445-2456; Ohage and Steipe (1999) *J. Mol. Biol.* **291**:1119-1128; Ohage et al. (1999) *J. Mol. Biol.* **291**:1129-1134; Wirtz and Steipe (1999) *Protein Sci.* **8**:2245-2250; Zhu et al. (1999) *J. Immunol. Methods*, **231**:207-222.

XenoMouse Technology Antibodies in accordance with the invention are preferably pre0pared by the utilization of a transgenic mouse that has a substantial portion of the human antibody producing genome inserted, but that is rendered deficient in the production of endogenous murine antibodies (e.g., XenoMouse strains available from Abgenix Inc., Fremont, CA). Such mice are capable of producing human immunoglobulin molecules and antibodies and are virtually deficient in the production of murine immunoglobulin molecules and antibodies. Technologies utilized for achieving the same are disclosed in the patents, applications, and references disclosed herein.

The ability to clone and reconstruct megabase-sized human loci in YACs and to introduce them into the mouse germline provides a powerful approach to elucidating the functional components of very large or crudely mapped loci, as well as generating useful models of human disease. Furthermore, the utilization of such technology for substitution of mouse loci

with their human equivalents could provide unique insights into the expression and regulation of human gene products during development, their communication with other systems, and their involvement in disease induction and progression. An important practical application of such a strategy is the "humanization" of the mouse humoral immune system. Introduction of human immunoglobulin (Ig) loci into mice in which the endogenous Ig genes have been inactivated offers the opportunity to study the mechanisms underlying programmed expression and assembly of antibodies as well as their role in B cell development. Furthermore, such a strategy could provide an ideal source for the production of fully human monoclonal antibodies: an important milestone toward fulfilling the promise of antibody therapy in human disease.

Fully human antibodies are expected to minimize the immunogenic and allergic responses intrinsic to mouse or mouse-derivatized monoclonal antibodies and thus to increase the efficacy and safety of the administered antibodies. The use of fully human antibodies can be expected to provide a substantial advantage in the treatment of chronic and recurring human diseases, such as cancer, which require repeated antibody administrations.

One approach toward this goal was to engineer mouse strains deficient in mouse antibody production to harbor large fragments of the human Ig loci in anticipation that such mice would produce a large repertoire of human antibodies in the absence of mouse antibodies. Large human Ig fragments would preserve the large variable gene diversity as well as the proper regulation of antibody production and expression. By exploiting the mouse machinery for antibody diversification and selection and the lack of immunological tolerance to human proteins, the reproduced human antibody repertoire in these mouse strains should yield high affinity antibodies against any antigen of interest, including human antigens. Using the hybridoma technology, antigen-specific human monoclonal antibodies with the desired specificity could be readily produced and selected.

This general strategy was demonstrated in connection with the generation of the first "XenoMouseT" strains as published in 1994. See

Green et al. (1994) *Nature Genetics*, 7:13-21. The XenoMouse strains were engineered with yeast artificial chromosomes (YACS) containing 245-kb and 10,190-kb-sized germline configuration fragments of the human heavy chain locus and kappa light chain locus, respectively, which contained core variable and constant region sequences. *Id.* The human Ig containing YACs proved to be compatible with the mouse system for both rearrangement and expression of antibodies and were capable of substituting for the inactivated mouse Ig genes. This was demonstrated by their ability to induce B-cell development, to produce an adult-like human repertoire of fully human antibodies, and to generate antigen-specific human monoclonal antibodies. These results also suggested that introduction of larger portions of the human Ig loci containing greater numbers of V genes, additional regulatory elements, and human Ig constant regions might recapitulate substantially the full repertoire that is characteristic of the human humoral response to infection and immunization. The work of Green et al. was recently extended to the introduction of greater than approximately 80% of the human antibody repertoire through the use of megabase-sized, germline configuration YAC fragments of the human heavy chain loci and kappa light chain loci, respectively, to produce XenoMouse mice. See Mendez et al. (1997) *Nature Genetics*, **15**:146-156; Green and Jakobovits (1998) *J. Exp. Med.* **188**:483-495; and Green (1999) *J. Immunol. Methods*, **231**:11-23, the disclosures of which are hereby incorporated herein by reference.

Human anti-mouse antibody (HAMA) responses have led the industry to prepare chimeric or otherwise humanized antibodies. While chimeric antibodies typically are comprised of a human constant region and a murine variable region, it is expected that certain human anti-chimeric antibody (HACA) responses will be observed, particularly in treatments involving chronic or multi-dose utilizations of the antibody. Thus, it is desirable to provide fully human antibodies against B7-related polypeptides of the invention in order to vitiate concerns and/or effects of HAMA or HACA responses.

Polypeptide antibodies of the invention may be chemically synthesized or produced through the use of recombinant expression systems. Accordingly, the invention further embraces polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention also encompasses polynucleotides that hybridize under stringent or lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, an antibody that specifically binds to a polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of one or more of the B7-related sequences as set forth in **Figures 1-6.**

The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody can be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al. (1994) *BioTechniques*, **17**:242), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, the annealing and ligating of those oligonucleotides, and then the amplification of the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody can be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin can be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, (or a nucleic acid, preferably poly(A)$^+$ RNA, isolated from), any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence. Alternatively, cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody

can be employed. Amplified nucleic acids generated by PCR can then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence and corresponding amino acid sequence of the antibody are determined, the nucleotide sequence of the antibody can be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al. (1990) *Molecular Cloning, A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY; and Ausubel et al., eds., (1998) *Current Protocols in Molecular Biology*, John Wiley & Sons, NY, which are both incorporated by reference herein in their entireties), to generate antibodies having a different amino acid sequence, for example, to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light chain variable domains can be inspected to identify the sequences of the CDRs by methods that are well known in the art, e.g., by comparison to known amino acid sequences of other heavy and light chain variable regions, to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs can be inserted within framework regions, e.g., into human framework regions, to humanize a non-human antibody, as described *supra*. The framework regions can be naturally occurring or consensus framework regions, and preferably, are human framework regions (see, e.g., Chothia et al. (1998) *J. Mol. Biol.* **278**:457-479 for a listing of human framework regions).

Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds to a B7-related polypeptide of the invention. Also preferably, as discussed *supra*, one or more amino acid substitutions can be made within the framework regions; such amino acid substitutions are performed with the goal of improving binding of the antibody to its antigen. In addition, such methods can be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond

to generate antibody molecules lacking one or more intrachain disulfide bonds. Other alterations to the polynucleotide are encompassed by the present invention and are within the skill of the art.

For some uses, such as for *in vitro* affinity maturation of an antibody of the invention, it is useful to express the V_H and V_L domains of the heavy and light chains of one or more antibodies of the invention as single chain antibodies, or Fab fragments, in a phage display library using phage display methods as described *supra*. For example, the cDNAs encoding the V_H and V_L domains of one or more antibodies of the invention can be expressed in all possible combinations using a phage display library, thereby allowing for the selection of V_H/V_L combinations that bind to the B7-related polypeptides according to the present invention with preferred binding characteristics such as improved affinity or improved off rates. In addition, V_H and V_L segments, particularly, the CDR regions of the V_H and V_L domains of one or more antibodies of the invention, can be mutated *in vitro*. Expression of V_H and V_L domains with "mutant" CDRs in a phage display library allows for the selection of V_H/V_L combinations that bind to B7-related polypeptides of the invention with preferred binding characteristics such as improved affinity or improved off rates.

In phage display methods, functional antibody domains are displayed on the surface of phage particles that carry the polynucleotide sequences encoding them. In particular, DNA sequences encoding the V_H and V_L domains are amplified from animal cDNA libraries (e.g., human or murine cDNA libraries of lymphoid tissues) or from synthetic cDNA libraries. The DNA encoding the V_H and V_L domains are joined together by an scFv linker by PCR and cloned into a phagemid vector (e.g., p CANTAB 6 or pComb 3 HSS). The vector is introduced into *E. coli* via electroporation and the *E. coli* is infected with helper phage. Phage used in these methods are typically filamentous phage, including fd and M13, and the V_H and V_L domains are usually recombinantly fused either to the phage gene III or gene VIII. Phage expressing an antigen binding domain that binds to an antigen of interest (i.e., a B7-related polypeptide of the invention or a fragment thereof)

can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured onto a solid surface or bead.

The antibodies according to the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis, by intracellular immunization (i.e., intrabody technology), or preferably, by recombinant expression techniques. Methods of producing antibodies include, but are not limited to, hybridoma technology, EBV transformation, and other methods discussed herein as well as through the use recombinant DNA technology, as discussed below.

Recombinant expression of an antibody of the invention, or fragment, derivative, variant or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the antibody molecule can be produced by recombinant DNA technology using techniques well known in the art. Methods for preparing a protein by expressing a polynucleotide encoding an antibody are described herein. Methods that are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. The invention, thus embraces replicable vectors comprising a nucleotide sequence encoding an antibody molecule of the invention, or a heavy or light chain thereof, or a heavy or light chain variable domain, operably linked to a promoter. Such vectors can include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody can be cloned into such a vector for expression of the entire heavy or light chain.

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host expression vector systems can be utilized to express the antibody molecules of the invention. Such expression systems represent vehicles by which the coding sequences of interest can be expressed, their encoded products produced and subsequently purified. These systems also represent cells that can, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule of the invention *in situ*. Cell expression systems include, but are not limited, to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., *Saccharomyces* or *Pichia*) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus (CaMV) or tobacco mosaic virus (TMV)), transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3, NSO cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as *E. coli*, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecules,

are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary (CHO) cells, in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus, is an effective expression system for antibodies (Foecking et al. (1986) *Gene*, **45**:101; Cockett et al. (1990) *BioTechnology*, **8**:2).

In bacterial systems, a number of expression vectors can be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced for the generation of pharmaceutical compositions of an antibody molecule, for example, vectors that direct the expression of high levels of fusion protein products that are readily purified are often desirable. Such vectors include, but are not limited to, the *E. coli* expression vector pUR278 (Ruther et al. (1983) *EMBO J.* **2**:1791), in which the antibody coding sequence can be ligated individually into the vector in-frame with the lacZ coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye (1985) *Nucleic Acids Res.* **13**:3101-3109; Van Heeke & Schuster (1989) *J. Biol. Chem.* **24**:5503-5509; and the like). pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, *Autographa californica* nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in *Spodoptera figuriperda* cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

In mammalian host cells, a number of viral based

expression systems can be utilized. In cases in which an adenovirus is used as an expression vector, the antibody coding sequence of interest can be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene can then be inserted in the adenovirus genome *by in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (e.g., region El or E3) results in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (See, e.g., Logan and Shenk (1984) *Proc. Natl. Acad. Sci. USA*, **81**:355-359). Specific initiation signals can also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in-phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression can be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al. (1987) *Methods in Enzymol.* **153**:51-544).

In addition, a host cell strain can be chosen to modulate the expression of the inserted sequences, or modify and process the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products can be important for the function of the protein.

Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells that possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product can be used. Such mammalian host cells include, but are not limited to, CHO, VERY, BHK, HeLa, COS, MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T,

HTB2, BT20 and T47D, and normal mammary gland cell lines such as, for example, CRL7030 and Hs578Bst.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines that stably express the antibody molecule can be engineered. Rather than using expression vectors that contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoters, enhancer sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, such genetically engineered cells can be allowed to grow for 1-2 days in an enriched medium, and then are typically replated in a selective medium. A selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which, in turn, can be cloned and expanded into cell lines. This method can advantageously be used to engineer cell lines expressing the antibody molecule. Such engineered cell lines are particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

A number of selection systems can be used, including but not limited to, herpes simplex virus thymidine kinase (HSV TK), (Wigler et al. (1977) *Cell*, **11**:223), hypoxanthine-guanine phosphoribosyltransferase (HGPRT), (Szybalska and Szybalski (1992) *Proc. Natl. Acad. Sci. USA*, **48**:202), and adenine phosphoribosyltransferase (Lowy et al. (1980) *Cell*, **22**:817) genes can be employed in tk-, hgprt-, or aprt- cells (APRT), respectively.

In addition, anti-metabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al. (1980) *Proc. Natl. Acad. Sci. USA*, **77**:357; and O'Hare et al. (1981) *Proc. Natl. Acad. Sci. USA*, **78**:1527); gpt, which confers resistance to mycophenolic acid (Mulligan and Berg (1981) *Proc. Natl. Acad. Sci. USA*, **78**:2072); neo, which confers resistance to the aminoglycoside G418 (*Clinical Pharmacy*, 12:488-505; Wu and Wu (1991) *Biotherapy*, **3**:87-

95; Tolstoshev (1993) *Ann. Rev. Pharmacol. Toxicol.* **32**:573-596; Mulligan (1993) *Science*, **260**:926-932; Anderson (1993) *Ann. Rev. Biochem.* **62**:191-21; May (1993) *TIB TECH*, **11**(5):155-215; and hygro, which confers resistance to hygromycin (Santerre et al. (1984) *Gene*, **30**:147). Methods commonly known in the art of recombinant DNA technology can be routinely applied to select the desired recombinant clone; such methods are described, for example, in Ausubel et al., eds., (1990) *Current Protocols in Molecular Biology*, John Wiley & Sons, NY; Kriegler (1990) *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY; in Chapters 12 and 13, Dracopoli et al., eds., (1994) *Current Protocols in Human Genetics*, John Wiley & Sons, NY; Colberre-Garapin et al. (1981) *J. Mol. Biol.* **150**:1, which are incorporated by reference herein in their entireties.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel (1987) *The Use of Vectors Based on Gene Amplification for the Expression of Cloned Genes in Mammalian Cells In DNA Cloning*, Vol. 3. Academic Press, New York). When a marker in the vector system expressing an antibody is amplifiable, an increase in the level of inhibitor present in the host cell culture will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al. (1983) *Mol. Cell. Biol.* **3**:257).

Vectors that use glutamine synthase (GS) or DHFR as the selectable markers can be amplified in the presence of the drugs methionine sulphoximine or methotrexate, respectively. An advantage of glutamine synthase based vectors is the availability of cell lines (e.g., the murine myeloma cell line, NSO) which are glutamine synthase negative. Glutamine synthase expression systems can also function in glutamine synthase expressing cells (e.g. Chinese Hamster Ovary (CHO) cells) by providing additional inhibitor to prevent the functioning of the endogenous gene.

Vectors that express glutamine synthase as the selectable marker include, but are not limited to, the pEE6 expression vector (described in Stephens and Cockett (1989) *Nucl. Acids. Res.* **17**:7110). A glutamine

synthase expression system and components thereof are detailed in PCT publications: W087/04462; W086/05807; W089/01036; W089/10404; and W091/06657, which are incorporated by reference herein in their entireties. In addition, glutamine synthase expression vectors that can be used in accordance with the present invention are commercially available from suppliers, including, for example, Lonza Biologics, Inc. (Portsmouth, NH). The expression and production of monoclonal antibodies using a GS expression system in murine myeloma cells has been described (Bebbington et al. (1992) *BioTechnology*, **10**:169 and in Biblia and Robinson (1995) *Biotechnol. Prog.* **11**:1, which are incorporated by reference herein in their entireties).

A host cell can be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors can contain identical selectable markers, which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector can be used which encodes, and is capable of expressing, both the heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot (1986) *Nature*, **322**:52; Kohler (1980) *Proc. Natl. Acad. Sci. USA*, **77**:2197). The coding sequences for the heavy and light chains can comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it can be purified by any method known in the art for the purification of an immunoglobulin or polypeptide molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen, Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art, to facilitate purification.

The present invention encompasses antibodies that are recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugated) to a polypeptide (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 contiguous amino acids of the polypeptide) of the present invention, such as BSL2 (e.g., **SEQ ID NO:**3, 5, or 7), to generate fusion proteins. The fusion does not necessarily need to be direct, but can occur through linker sequences. The antibodies can be specific for antigens other than polypeptides (or portions thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 contiguous amino acids of the polypeptide) of the present invention. For example, antibodies can be used to target the polypeptides of the present invention to particular cell types, either *in vitro* or *in vivo*, by fusing or conjugating the polypeptides of the present invention to antibodies specific for particular cell surface receptors.

Polypeptides and/or antibodies of the present invention (including fragments or variants thereof) can be fused to either the N-terminal or C-terminal end of the heterologous protein (e.g., immunoglobulin Fc polypeptide or human serum albumin polypeptide). Antibodies of the invention can also be fused to albumin (including, but not limited to, recombinant human serum albumin (see, e.g., U.S. Patent No. 5,876,969, issued March 2, 1999; EP Patent 0 413 622; and U.S. Patent No. 5,766,883, issued June 16, 1998, incorporated herein by reference in their entirety), resulting in chimeric polypeptides. In a preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with the mature form of human serum albumin (i.e., amino acids 1-585 of human serum albumin as shown in Figures 1 and 2 of EP Patent 0 322 094, which is herein incorporated by reference in its entirety). In another preferred embodiment, polypeptides and/or antibodies of the present invention (including fragments or variants thereof) are fused with polypeptide fragments comprising, or alternatively consisting of, amino acid residues 1-z of human serum albumin, where z is an integer from 369 to 419, as described in U.S. Patent No. 5,766,883 incorporated herein by reference in its entirety.

BSL2 (e.g., **SEQ ID NO:**8, 10, or 12) polynucleotides encoding

fusion proteins, and antibodies to these fusion proteins, are also encompassed by the invention. Such fusion proteins may, for example, facilitate purification and may increase half-life *in vivo*. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in *in vitro* immunoassays and purification methods using methods known in the art. See, e.g., Harbor et al., *supra*, and PCT publication WO 93/21232; EP 439, 095; Naramura et al. (1994) *Immunol. Lett.* **39**:91-99; U.S. Patent No. 5,474,981; Gillies et al. (1992) *Proc. Natl. Acad. Sci. USA*, **89**:1428-1432; Fell et al. (1991) *J. Immunol.* **146**:2446-2452, which are incorporated by reference herein in their entireties. Antibodies to BSL2 (e.g., **SEQ ID NO:**9, 11, or 13) fusion proteins can be used in any of the antibody-based methods for polypeptide identification, purification, and for antibody-format assays for diagnosis, treatment, and monitoring known in the art and/or disclosed herein.

The present invention further includes compositions comprising the B7-related polypeptides of the present invention fused or conjugated to antibody domains other than the variable region domain. For example, the polypeptides of the present invention can be fused or conjugated to an antibody Fc region, or portion thereof. The antibody portion fused to a polypeptide of the present invention can comprise the constant region, hinge region, CH1 domain, CH2 domain, CH3 domain, or any combination of whole domains or portions thereof. The polypeptides can also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the art. (See, e.g., U.S. Patent Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al. (1991) *Proc. Natl. Acad. Sci. USA*, **88**:10535-10539; Zheng et al. (1995) *J. Immunol.* **154**:5590-5600; and Vil et al., *Proc. Natl. Acad. Sci. USA*, **89**:11337-11341, which are hereby incorporated by reference herein in their entireties).

As discussed *supra*, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of one or more of a B7-related amino acid sequence as set forth in **Figures 1-6** can be fused or conjugated to the above antibody portions to increase the *in vivo* half life of the polypeptides, or for use in immunoassays using methods known in the art. Further, the polypeptides corresponding to one or more of the B7-related sequences as set forth in **Figures 1-6** can be fused or conjugated to the above antibody portions to facilitate purification. For guidance, chimeric proteins having the first two domains of the human CD4 polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins have been described. (EP 394,827; Traunecker et al. (1988) *Nature*, **331**:84-86). The polypeptides of the present invention fused or conjugated to an antibody, or portion thereof, having disulfide-linked dimeric structures (due to the IgG), for example, can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al. (1995) *J. Biochem.* **270**:3958-3964). In many cases, the Fc portion in a fusion protein is beneficial in therapy, diagnosis, and/or screening methods, and thus can result in, for example, improved pharmacokinetic properties. (EP A 232, 262). In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, Bennett et al. (1995) *J. Molecular Recognition*, **8**:52-58; and Johanson et al. (1995) *J. Biol. Chem.* **270**:9459-9471). Alternatively, deleting the Fc portion after the fusion protein has been expressed, detected, and purified, may be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations.

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide, to facilitate their purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., Chatsworth, CA), among others, many of which are

commercially available. As described in Gentz et al. (1989) *Proc. Natl. Acad. Sci. USA*, **86**:821-824, for instance, hexa histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin (HA) protein (Wilson et al. (1984) *Cell*, **37**:767) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing procedure, for example, to determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Nonlimiting examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance can be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. (See, for example, U.S. Patent No. 4,741,900 for metal ions that can be conjugated to antibodies for use as diagnostics according to the present invention).

Nonlimiting examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; nonlimiting examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; nonlimiting examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; a nonlimiting example of a luminescent material includes luminol; nonlimiting examples of bioluminescent materials include luciferase, luciferin, and aequorin; and nonlimiting examples of suitable radioactive material include iodine (^{125}I, ^{131}I), carbon (^{14}C), sulfur (3sus), tritium (^{3}H),

indium (^{111}In and other radioactive isotopes of inidium), technetium (^{99}Tc, ^{99m}Tc), thallium (20'Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{19}F),^{153}Sm, ^{177}Lu, Gd, radioactive Pm, radioactive La, radioactive Yb, ^{166}Ho,^{90}Y, radioactive Sc, radioactive Re, radioactive Re, ^{142}Pr, ^{105}Rh, and ^{97}Ru.

In specific embodiments, the B7-related polypeptides of the invention are attached to macrocyclic chelators useful for conjugating radiometal ions, including, but not limited to, ^{111}In, ^{177}Lu, ^{90}Y, ^{166}Ho, and ^{153}Sm, to polypeptides. In a preferred embodiment, the radiometal ion associated with the macrocyclic chelators attached to the B7-related polypeptides of the invention is ^{111}In. In another preferred embodiment, the radiometal ion associated with the macrocyclic chelator attached to the B7-related polypeptides of the invention is ^{90}Y. In specific embodiments, the macrocyclic chelator is 1, 4, 7, 10-tetraazacyclododecane-N, N', N", N"'-tetraacetic acid (DOTA). In other specific embodiments, the DOTA is attached to the B7-related polypeptides of the invention via a linker molecule.

Examples of linker molecules useful for conjugating DOTA to a polypeptide are commonly known in the art. (See, for example, DeNardo et al. (1998) *Clin. Cancer Res.* 4(10):2483-90; Peterson et al. (1999) *Bioconjug. Chem.* **10**(4):553-557; and Zimmerman et al. (1999) *Nucl. Med. Biol.* **26**(8): 943-950, which are hereby incorporated by reference in their entirety. In addition, U.S. Patent Nos. 5,652,361 and 5,756,065, which disclose chelating agents that can be conjugated to antibodies and methods for making and using them, are hereby incorporated by reference in their entireties. Though U.S. Patent Nos. 5,652,361 and 5,756,065 focus on conjugating chelating agents to antibodies, one skilled in the art can readily adapt the methods disclosed therein in order to conjugate chelating agents to other polypeptides.

Antibodies can also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Techniques for conjugating therapeutic moieties to antibodies

are well known, see, e.g., Amon et al. (1985) "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al., eds., Alan R. Liss, Inc., pp. 243-56; Hellstrom et al. (1987) "Antibodies For Drug Delivery", *Controlled Drug Delivery*, 2nd Ed., Robinson et al. (eds.), Marcel Deldcer, Inc., pp. 623-53; Thorpe, (1985) "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al., eds., pp. 475-506; Baldwin et al., eds., (1985) "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", *Monoclonal Antibodies For Cancer Detection And Therapy*, Academic Press, pp. 303-316; and Thorpe et al. (1982) *Immunol. Rev.* **62**:119-158. Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate, e.g., as described in U.S. Patent No. 4,676,980 to Segal, which is incorporated herein by reference in its entirety. An antibody, i.e., an antibody specific for a B7-related polypeptide of this invention, with or without a therapeutic moiety conjugated to it, and administered alone or in combination with cytotoxic factor(s) and/or cytokine(s), can be used as a therapeutic.

The antibodies of the invention can be utilized for immunophenotyping of cell lines and biological samples. The translation product of the BSL2-encoding sequences of the present invention can be useful as cell specific marker(s), or more specifically, as cellular marker(s) that are differentially expressed at various stages of differentiation and/or maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, allow for the screening of cellular populations expressing the marker. Various techniques utilizing monoclonal antibodies can be employed to screen for cellular populations expressing the marker(s), including magnetic separation using antibody-coated magnetic beads, "panning" with antibody(ies) attached to a solid matrix (i.e., tissue culture plate), and flow cytometry (See, e.g., U.S. Patent No. 5,985,660; and Morrison et al. (1999) *Cell*, **96**:737-749).

These techniques allow for the screening of particular

populations of cells, such as might be found with hematological malignancies (i. e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might be found in human umbilical cord blood.

Antibodies according to this invention can be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include, but are not limited to, competitive and non-competitive assay systems using techniques such as BIAcore analysis, FACS (Fluorescence Activated Cell Sorter) analysis, immunofluorescence, immunocytochemistry, Western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assays),"sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known and practiced in the art (see, e.g., Ausubel et al, eds., (1994) *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by reference herein in its entirety). Nonlimiting, exemplary immunoassays are described briefly below.

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (i.e., 1% NP-40 or Triton X-100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1% Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate); adding the antibody of interest to the cell lysate; incubating for a period of time (e.g., 1 to 4 hr) at 4°C; adding protein A and/or protein G sepharose beads to the cell lysate; incubating for about 60 min or more at 4°C; washing the beads in lysis buffer; and resuspending the beads in SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, for example,

Western blot analysis. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding immunoprecipitation protocols, see, e.g., Ausubel et al, eds., (1994) *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York, at 10.16.1.

Western blot analysis generally comprises preparing protein samples; electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%-20% SDS PAGE depending on the molecular weight of the antigen); transferring the protein sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon; blocking the membrane in blocking solution (e.g., PBS with 3% BSA or nonfat milk); washing the membrane in washing buffer (e.g., PBS-Tween®20); blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer; washing the membrane in washing buffer; blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti-human antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., ^{32}P or ^{125}I) diluted in blocking buffer; washing the membrane in wash buffer; and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding Western blot protocols, see, e.g., Ausubel et al, eds. (1994) *Current Protocols in Molecular Biology*, Vol. 1, John Wiley & Sons, Inc., New York, at 10.8.1.

ELISAs comprise preparing antigen; coating the wells of a 96 well microtiter plate with antigen; adding to the wells the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase); incubating for a period of time; and detecting the presence of the antigen. In ELISAs, the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound can be added to the wells. Further, instead of coating

the wells with antigen, the antibody can be first coated onto the well. In this case, a second antibody conjugated to a detectable compound can be added to the antibody-coated wells following the addition of the antigen of interest. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected, as well as other variations of ELISAs known in the art.

In the initial steps, an ELISA assay may involve preparing an antibody specific to antigens of a B7-related polypeptide or peptide fragments thereof, preferably a monoclonal antibody. In addition, a reporter antibody can be used to recognize and bind to the monoclonal antibody. To the reporter antibody a detectable reagent may be attached, such as a radioactive isotope, a fluorescent moiety, or, in this example, an enzyme, such as horseradish peroxidase. To carry out an ELISA assay, a sample can be removed from a host, e.g., a patient sample, and incubated on a solid support, e.g., wells of a microtiter plate, or a polystyrene dish, to which the proteins in the sample can bind. Any free protein binding sites on the dish may then be blocked by incubating with a non-specific protein such as bovine serum albumin. The monoclonal antibody can then be added to the solid support, e.g., the wells or the dish, and allowed to incubate.

During the incubation time, the monoclonal antibodies may attach to any B7-related polypeptides or peptides that have attached to the polystyrene dish. All unbound monoclonal antibody can then be washed away using an appropriate buffer solution. The reporter antibody, e.g., linked to horseradish peroxidase, can be added to the support, thereby resulting in the binding of the reporter antibody to any monoclonal antibody that has bound to B7-related polypeptides or peptides that are present in the sample. Unattached reporter antibody can then be washed away. Peroxidase substrate can be added to the support and the amount of color developed in a given time period can be taken to provide a measurement of the amount of B7-related polypeptides or peptides that are present in a given volume of patient sample when compared against a standard curve. For further discussion regarding ELISAs, see, e.g., Ausubel et al, eds. (1994) *Current*

Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York, at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay involving the incubation of labeled antigen (e.g., ^{3}H or ^{125}I), or a fragment or variant thereof, with the antibody of interest in the presence of increasing amounts of labeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a B7-related polypeptide of the invention and the binding off rates can be determined from the data by Scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, a B7-related polypeptide such as BSL2 (e.g., **SEQ ID NO:3**, 5, or 7) is incubated with antibody of interest conjugated to a labeled compound (e.g., a compound labeled with ^{3}H or ^{125}I) in the presence of increasing amounts of an unlabeled second antibody. This kind of competitive assay between two antibodies, may also be used to determine if two antibodies bind to the same or different epitopes.

In a preferred embodiment, BIAcore kinetic analysis is used to determine the binding on and off rates of antibodies (including antibody fragments or variants thereof) to a B7-related polypeptide, or fragments or variants of a B7-related polypeptide disclosed herein. Kinetic analysis comprises analyzing the binding and dissociation of antibodies from chips with immobilized B7-related polypeptide such as BSL2 (e.g., **SEQ ID NO:**3, 5, or 7) on the chip surface.

Assays utilizing B7-related nucleic acids or polypeptides

Expression analysis of B7-related factors: Several well-established techniques can be used to determine the expression levels, patterns, and cell-type specificity of the B7-related factors. For example, mRNA levels can be determined utilizing Northern blot analysis (J.C. Alwine et al. (1977) *Proc. Natl. Acad. Sci. USA* **74**:5350-5354; I.M. Bird (1998) *Methods Mol. Biol.* **105**:325-36.), whereby poly(A)$^{+}$ RNA is isolated from cells,

separated by gel electrophoresis, blotted onto a support surface (e.g., nitrocellulose or Immobilon-Ny+ (Millipore Corp., Bedford, MA)), and incubated with a labeled (e.g., fluorescently labeled or radiolabeled) oligonucleotide probe that is capable of hybridizing with the mRNA of interest. Alternatively, mRNA levels can be determined by quantitative (for review, see W.M. Freeman et al. (1999) *Biotechniques* **26**:112-122) or semi-quantitative RT-PCR analysis (Ren et al. *Mol. Brain Res.* **59**:256-63). In accordance with this technique, poly(A)$^+$ RNA is isolated from cells, used for cDNA synthesis, and the resultant cDNA is incubated with PCR primers that are capable of hybridizing with the template and amplifying the template sequence to produce levels of the PCR product that are proportional to the cellular levels of the mRNA of interest. Another technique, *in situ* hybridization, can also be used to determine mRNA levels (reviewed by A.K. Raap (1998) *Mutat. Res.* **400**:287-298). *In situ* hybridization techniques allow the visual detection of mRNA in a cell by incubating the cell with a labeled (e.g., fluorescently labeled or digoxigenin labeled) oligonucleotide probe that hybridizes to the mRNA of interest, and then examining the cell by microscopy .

Chromosomal mapping of B7-related genes: The chromosomal location of B7-related genes can be determined by various techniques known in the art. For example, high-resolution chromosomal banding can be used (reviewed by M. Ronne (1990) *In Vivo* **4**:337-65). High-resolution banding techniques utilize elongated chromosomes from cells at early mitotic stages, which have been synchronized using DNA-synthesis inhibitors (e.g., methotrexate or thymidine) or DNA-binding agents (e.g., ethidium bromide). However, these techniques can only be used to map a gene to a relatively large region of a chromosome (~3 Mb). For more accurate gene mapping, fluorescence *in situ* hybridization (FISH) techniques can be used. In particular, high-resolution FISH techniques (A. Palotie et al. (1996) *Ann. Med.* **28**:101-106) utilize free chromatin, DNA fibers, or mechanically-stretched chromosomes to map gene sequences ranging from several kilobases to 300-kb in size. Alternatively, the chromosomal location of a gene can be determined from the appropriate genome database, for example, the *Homo*

sapiens genome database available at the Entrez Genome website (National Center for Biotechnology Information, Bethesda, MD).

Identification of T-cell ligands: The B7-related polypeptides or peptides disclosed herein can be used to identify their cognate ligands on immune or inflammatory response cells, such as T-cells (i.e., CD28- or CTLA-4-related ligands). Candidate ligands, or fragments derived therefrom, can be identified and analyzed by many well-known methods in the art (see T.E. Creighton, Ed. (1997) *Proteins Structure: A Practical Approach,* IRL Press at Oxford Press, Oxford, England). For example, T-cell ligands that bind to the B7-related polypeptides or peptides can be identified from extracts or lysates obtained from animal, preferably human, immune or inflammatory response cells (e.g., T-cells). The proteins obtained from these sources can be separated into bands using sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred by electroblotting, for example, onto a suitable solid-phase support or membrane (e.g., nitrocellulose or polyvinylidene fluoride (PVDF)). The solid-phase support or membrane can then be incubated with a labeled form of a B7-related polypeptide or peptide, e.g., BSL2 (e.g., **SEQ ID NO:**3, 5, or 7). Bands that exhibit specific binding with the labeled B7-related polypeptide or peptide can then be identified, isolated, purified, and analyzed by amino acid analysis and/or Edman degradation to determine the amino acid sequence of peptides derived therefrom.

As an alternative approach, a fusion protein comprising a B7-related polypeptide can be attached to a solid support and incubated with extracts obtained from cells, such as CHO or COS cells, that are transfected with an appropriate cDNA library. For example, a cDNA library can be constructed from resting or activated immortal human T-cell lines, such as CEM, HUT78, or Jurkat cell lines, or from resting or activated human T-cells derived from peripheral blood, tonsil, spleen, thymus or other specialized lymphoid tissues. Such cells can be activated by the addition of anti-CD3 and anti-CD28 monoclonal antibodies, phytohemaglutinin (PHA), or phorbol 12-myristate-13-acetate (PMA) with ionomycin. The cDNA library construct can

contain a removable epitope tag (see above) that is different from the fusion protein, and will facilitate purification of the library expression product(s) that associate with the fusion protein. The isolated library expression product(s) can then be isolated and characterized.

In addition, a fusion protein comprising a B7-related polypeptide can be attached to a solid support (e.g., a column comprising beads that specifically bind to the fusion protein) and incubated with lysates obtained from cells, such as T-cells, that are enriched for integral membrane proteins. The cellular proteins that associate with the fusion protein can be isolated and then characterized using MALDI-TOF analysis (Matrix Assisted Laser Desorption Ionization Time Of Flight Analysis; reviewed by Yates JR 3rd. (1998) *J. Mass Spectrom.* **33**:1-19; P. Chaurand et al. (1999) *J. Am. Soc. Mass Spectrom.* **10**:91-103). Fusion proteins can include, for example, FLAG®- (B.L. Brizzard et al. (1994) *Biotechniques* **16**:730-735), 6X-HIS, and GST fusion proteins (see above), which can be attached to solid supports that are conjugated with anti-FLAG® antibodies, nickel, or glutathione molecules, respectively. Methods of producing and purifying such fusion proteins are well known in the art.

Another suitable ligand-binding assay is the yeast two-hybrid system (Fields et al. (1989) *Nature* **340**:245-246; U.S. Patent No. 5,283,173). The two-hybrid system relies on the reconstitution of transcription activation activity by association of the DNA-binding and transcription activation domains of a transcriptional activator through protein-protein interaction. The yeast GAL4 transcriptional activator may be used in this way, although other transcription factors have been used and are well known in the art. To carryout the two-hybrid assay, the GAL4 DNA-binding domain and the GAL4 transcription activation domain are expressed, separately, as fusions to potential interacting polypeptides. For example, one fusion protein can comprise a B7-related polypeptide fused to the GAL4 DNA-binding domain. The other fusion protein can comprise, for example, a T-cell cDNA library encoded polypeptide fused to the GAL4 transcription activation domain. If the two, coexpressed fusion proteins interact in the nucleus of a host cell, a

reporter gene (e.g. LacZ) is activated to produce a detectable phenotype. The host cells that show two-hybrid interactions can be used to isolate the containing plasmids containing the cDNA library sequences. These plasmids can be analyzed to determine the nucleic acid sequence and predicted polypeptide sequence of the candidate T-cell ligand.

Related, *in vivo*, methods such as the three-hybrid (Licitra et al. (1996) *Proc. Natl. Acad. Sci. USA* **93**:12817-12821), and reverse two-hybrid (Vidal et al. (1996) *Proc. Natl. Acad. Sci. USA* **93**:10315-10320) systems may serve as alternative approaches. Commercially available two-hybrid systems such as the CLONTECH Matchmaker™ systems and protocols (CLONTECH, Palo Alto, CA) may be also be used. (See also, A.R. Mendelsohn et al. (1994) *Curr. Op. Biotech.* **5**:482; E.M. Phizicky et al. (1995) *Microbiological Rev.* **59**:94; M. Yang et al. (1995) *Nucleic Acids Res.* **23**:1152; S. Fields et al. (1994) *Trends Genet.* **10**:286; and U.S. Patent No. 6,283,173 and 5,468,614).

Ligand sequence(s) obtained from ligand-binding assay(s) can be compared with subject sequences in available databases such as, without limitation, GenPept, SWISS-PROT, and Incyte Genomics databases (Incyte Genomics). These databases, which contain previously identified and annotated sequences, may be searched for the full-length polypeptide and gene sequence using, for example, BLAST analysis (see above). In cases where the full-length sequences of the ligands are not available, extended or overlapping partial clones may be obtained by techniques conventionally known and practiced in the art. Non-limiting examples of such techniques include hybridization to plasmid or phage libraries of genomic DNA or cDNA; PCR from the same libraries using B7-related factor primer pairs; or hybridization or PCR directly to genomic DNA or cDNA. These clones may then be sequenced and assembled into full-length genes using the fragment sequence alignment program (PHRAP; Nickerson et al. (1997) *Nucleic Acids Res.* **25**:2745-2751).

Assays for B7-related factor activity: Screening the fragments, mutants or variants for those which retain characteristic B7-related polypeptide activity as described herein can be accomplished using one or

more of several different assays. For example, appropriate cells, such as CHO cells, can be transfected with the cloned variants and then analyzed for cell surface phenotype by indirect immunofluorescence and flow cytometry. Cell surface expression of the transfected cells is evaluated using a monoclonal antibody specifically reactive with a cell surface form of a B7-related factor (see above). Production of secreted forms of the B7-related factors can be evaluated by immunoprecipitation using a monoclonal antibody specifically reactive with a B7-related factor.

Other, more preferred, assays take advantage of the functional characteristics of the B7-related factors. As previously set forth, the binding of the B7-related factors to its T-cell ligand(s) causes the cells to produce increased levels of lymphokines, particularly of interleukin-2. Thus, B7-related factor function can be assessed by measuring the synthesis of lymphokines, such as interleukin-2 or other novel and as yet undefined cytokines, and/or assaying for T-cell proliferation by $CD28^+$ T-cells that have received a primary activation signal. Any one of several conventional assays for interleukin-2 can be employed (see C.B. Thompson (1989) *Proc. Natl. Acad. Sci. USA* **86**:1333).

The same basic functional assays can also be used to screen for B7-related polypeptides, peptides, fusion proteins, or antibodies that block T-cell activation. The ability of such proteins to block the normal costimulatory signal and induce a state of anergy can be determined using subsequent attempts at stimulation of the T-cells with antigen presenting cells that express cell surface B cell activation antigen B7 and present antigen. If the T-cells are unresponsive to the activation attempts, as determined by IL-2 synthesis and T-cell proliferation, a state of anergy has been induced and can be determined by methods known in the art (see R.H. Schwartz (1990) *Science* **248**:1349-1356).

Modulators of B7-related factors

The BSL2 polypeptides, polynucleotides, variants, or fragments thereof, can be used to screen for test agents (e.g., agonists, antagonists, or inhibitors) that modulate the levels or activity of the corresponding B7-related

polypeptide. In addition, B7-related molecules can be used to identify endogenous modulators that bind to BSL2 polypeptides or polynucleotides in the cell. In one aspect of the present invention, the full-length BSL2 (e.g., **SEQ ID NO:**3, 5, or 7) polypeptide is used to identify modulators. Alternatively, variants or fragments of a BSL2 polypeptide are used. Such fragments may comprise, for example, one or more domains of the B7-related polypeptide (e.g., the extracellular and transmembrane domains) disclosed herein. Of particular interest are screening assays that identify agents that have relatively low levels of toxicity in human cells. A wide variety of assays may be used for this purpose, including *in vitro* protein-protein binding assays, electrophoretic mobility shift assays, immunoassays, and the like.

The term "modulator" as used herein describes any test agent, molecule, protein, peptide, or compound with the capability of directly or indirectly altering the physiological function, stability, or levels of the BSL2 polypeptide. Modulators that bind to the B7-related polypeptides or polynucleotides of the invention are potentially useful in diagnostic applications and/or pharmaceutical compositions, as described in detail herein. Test agents useful as modulators may encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Such molecules can comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. Test agents which can be used as modulators often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Test agents can also comprise biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof.

Test agents finding use as modulators may include, for example, 1) peptides such as soluble peptides, including Ig-tailed fusion peptides and members of random peptide libraries (see, e.g., Lam et al. (1991) *Nature*

354:82-84; Houghten et al. (1991) *Nature* **354**:84-86) and combinatorial chemistry-derived molecular libraries made of D- and/or L-configuration amino acids; 2) phosphopeptides (e.g., members of random and partially degenerate, directed phosphopeptide libraries, see, e.g., Songyang et al., (1993) *Cell* **72**:767-778); 3) antibodies (e.g., polyclonal, monoclonal, humanized, anti-idiotypic, chimeric, and single chain antibodies as well as Fab, $F(ab')_2$, Fab expression library fragments, and epitope-binding fragments of antibodies); and 4) small organic and inorganic molecules.

Test agents and modulators can be obtained from a wide variety of sources including libraries of synthetic or natural compounds. Synthetic compound libraries are commercially available from, for example, Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich Chemical Company, Inc. (Milwaukee, WI). Natural compound libraries comprising bacterial, fungal, plant or animal extracts are available from, for example, Pan Laboratories (Bothell, WA). In addition, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides.

Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts can be readily produced. Methods for the synthesis of molecular libraries are readily available (see, e.g., DeWitt et al. (1993) *Proc. Natl. Acad. Sci. USA* **90**:6909; Erb et al. (1994) *Proc. Natl. Acad. Sci. USA* **91**:11422; Zuckermann et al. (1994) *J. Med. Chem.* **37**:2678; Cho et al. (1993) *Science* **261**:1303; Carell et al. (1994) *Angew. Chem. Int. Ed. Engl.* **33**:2059; Carell et al. (1994) *Angew. Chem. Int. Ed. Engl.* **33**:2061; and in Gallop et al. (1994) *J. Med. Chem.* **37**:1233). In addition, natural or synthetic compound libraries and compounds can be readily modified through conventional chemical, physical and biochemical means (see, e.g., Blondelle et al. (1996) *Trends in Biotech.* **14**:60), and may be used to produce combinatorial libraries. In another approach, previously identified pharmacological agents can be subjected to directed or random chemical

modifications, such as acylation, alkylation, esterification, amidification, and the analogs can be screened for BSL2-modulating activity.

Numerous methods for producing combinatorial libraries are known in the art, including those involving biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer, or small molecule libraries of compounds (K. S. Lam (1997) *Anticancer Drug Des.* **12**:145).

Libraries may be screened in solution (e.g., Houghten, (1992) *Biotechniques* **13**:412-421), or on beads (Lam, (1991) *Nature* **354**:82-84), chips (Fodor, (1993) *Nature* **364**:555-556), bacteria or spores (Ladner U.S. Pat. No. 5,223,409), plasmids (Cull et al. (1992) *Proc. Natl. Acad. Sci. USA* **89**:1865-1869), or on phage (Scott and Smith, (1990) *Science* **249**:386-390; Devlin (1990) *Science* **249**:404-406; Cwirla et al. (1990) *Proc. Natl. Acad. Sci. USA* **97**:6378-6382; Felici (1991) *J. Mol. Biol.* **222**:301-310; Ladner, *supra*).

Where the screening assay is a binding assay, a BSL2 polypeptide, fusion protein, polynucleotide, analog, or fragment thereof, may be joined to a label, where the label can directly or indirectly provide a detectable signal. Various labels include radioisotopes, fluorescers, chemiluminescers, enzymes, specific binding molecules, particles, e.g. magnetic particles, and the like. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin, etc. For the specific binding members, the complementary member would normally be labeled with a molecule that provides for detection, in accordance with known procedures.

A variety of other reagents may be included in the screening assay. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc., that are used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Reagents that improve the efficiency of the assay, such as protease inhibitors, nuclease

inhibitors, anti-microbial agents, etc., may be used. The components are added in any order that produces the requisite binding. Incubations are performed at any temperature that facilitates optimal activity, typically between 4° and 40°C. Incubation periods are selected for optimum activity, but may also be optimized to facilitate rapid high-throughput screening. Normally, between 0.1 and 1 hour will be sufficient. In general, a plurality of assay mixtures is run in parallel with different agent concentrations to obtain a differential response to these concentrations. Typically, one of these concentrations serves as a negative control, i.e. at zero concentration or below the level of detection.

To perform cell-free screening assays, it may be desirable to immobilize either a BSL2 polypeptide, polynucleotide, or fragment to a surface to facilitate identification of modulators that bind to these molecules, as well as to accommodate automation of the assay. For example, a fusion protein comprising a BSL2 (e.g., **SEQ ID NO:**3, 5, or 7) polypeptide and an affinity-tag can be produced as described in detail herein. In one embodiment, a GST-fusion protein comprising a BSL2 polypeptide is adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione-derivatized microtiter plates. Cell lysates (e.g., containing ^{35}S-labeled polypeptides) are added to the polypeptide-coated beads under conditions to allow complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the polypeptide-coated beads are washed to remove any unbound polypeptides, and the amount of immobilized radiolabel is determined. Alternatively, the complex is dissociated and the radiolabel present in the supernatant is determined. In another approach, the beads are analyzed by SDS-PAGE to identify BSL2-binding polypeptides.

Various binding assays can be used to identify agonist or antagonists that alter the function or levels of a BSL2 (e.g., **SEQ ID NO:**3, 5, or 7) polypeptide. Such assays are designed to detect the interaction of test agents with BSL2 polypeptides, polynucleotides, functional equivalents, or fragments thereof. Interactions may be detected by direct measurement of binding. Alternatively, interactions may be detected by indirect indicators of

binding, such as stabilization/destabilization of protein structure, or activation/inhibition of biological function. Non-limiting examples of useful binding assays are detailed below.

Modulators that bind to BSL2 polypeptides, polynucleotides, functional equivalents, or fragments thereof, can be identified using real-time Bimolecular Interaction Analysis (BIA; Sjolander et al. (1991) *Anal. Chem.* **63**:2338-2345; Szabo et al. (1995) *Curr. Opin. Struct. Biol.* **5**:699-705; e.g., BIAcore™; LKB Pharmacia, Sweden). Modulators can also be identified by scintillation proximity assays (SPA, described in U.S. Patent No. 4,568,649). Binding assays using mitochondrial targeting signals (Hurt et al. (1985) *EMBO J.* **4**:2061-2068; Eilers and Schatz, (1986) *Nature* **322**:228-231) a plurality of defined polymers synthesized on a solid substrate (Fodor et al. (1991) *Science* **251**:767-773) may also be employed.

Two-hybrid systems may be used to identify modulators (see, e.g., U.S. Pat. No. 5,283,317; Zervos et al. (1993) *Cell* **72**:223-232; Madura et al. (1993) *J. Biol. Chem.* **268**:12046-12054; Bartel et al. (1993) *Biotechniques* **14**:920-924; Iwabuchi et al. (1993) *Oncogene* **8**:1693-1696; and Brent WO 94/10300). Alternatively, three-hybrid (Licitra et al. (1996) *Proc. Natl. Acad. Sci. USA* **93**:12817-12821), and reverse two-hybrid (Vidal et al. (1996) *Proc. Natl. Acad. Sci. USA* **93**:10315-10320) systems may be used. Commercially available two-hybrid systems such as the CLONTECH Matchmaker™ systems and protocols (CLONTECH Laboratories, Inc., Palo Alto, CA) are also useful (see also, A.R. Mendelsohn et al. (1994) *Curr. Op. Biotech.* **5**:482; E.M. Phizicky et al. (1995) *Microbiological Rev.* **59**:94; M. Yang et al. (1995) *Nucleic Acids Res.* **23**:1152; S. Fields et al. (1994) *Trends Genet.* **10**:286; and U.S. Patent No. 6,283,173 and 5,468,614).

Several methods of automated assays have been developed in recent years so as to permit screening of tens of thousands of test agents in a short period of time. High-throughput screening methods are particularly preferred for use with the present invention. The binding assays described herein can be adapted for high-throughput screens, or alternative screens may be employed. For example, continuous format high throughput screens

(CF-HTS) using at least one porous matrix allows the researcher to test large numbers of test agents for a wide range of biological or biochemical activity (see U.S. Patent No. 5,976,813 to Beutel et al.). Moreover, CF-HTS can be used to perform multi-step assays.

Diagnostics

According to another embodiment of the present invention, the B7-related polynucleotides, or fragments thereof, may be used for diagnostic purposes. The B7-related polynucleotides that may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6) polynucleotides, or fragments thereof, can be used to quantitate levels of BSL2 mRNA in biological samples in which expression (or under- or overexpression) of BSL2 polynucleotide may be correlated with disease. The diagnostic assay may be used to distinguish between the absence, presence, increase, and decrease of the expression of BSL2, and to monitor regulation of BSL2 polynucleotide levels during therapeutic treatment or intervention.

In one aspect, PCR probes can be used to detect B7-related polynucleotide sequences, including BSL2 genomic DNA sequences and BSL2-related nucleic acid sequences. The specificity of the probe, whether it is made from a highly specific region, e.g., at least 8 to 10 or 12 or 15 contiguous nucleotides in the 5' regulatory region, or a less specific region, e.g., especially in the 3' coding region, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low) will determine whether the probe identifies only naturally occurring sequences encoding the B7-related polypeptide, alleles thereof, or related sequences.

Probes may also be used for the detection of BSL2-related sequences, and should preferably contain at least 60%, preferably greater than 90%, identity to a BSL2 polynucleotide (e.g., **SEQ ID NO:**1, 2, 4, or 6), or a complementary sequence, or fragments thereof. The probes of this invention may be DNA or RNA, the probes may comprise all or a fragment of the nucleotide sequence of BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6), or a

complementary sequence thereof, and may include promoter, enhancer elements, and introns of the naturally occurring BSL2 polynucleotide.

Methods for producing specific probes for B7-related polynucleotides include the cloning of nucleic acid sequences of BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6), or a fragment thereof, into vectors for the production of mRNA probes. Such vectors are known in the art, commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a variety of detector/reporter groups, e.g., radionucleotides such as ^{32}P or ^{35}S, or enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

A wide variety of labels and conjugation techniques are known and employed by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding a BSL2 polypeptide include oligo-labeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, BSL2 polynucleotide sequences, or any portions or fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by addition of an appropriate RNA polymerase, such as T7, T3, or SP(6) and labeled nucleotides. These procedures may be conducted using a variety of commercially available kits (e.g., from Amersham Pharmacia Biotech, Inc., Piscataway, NJ; Promega Corp., Madison WI; and U.S. Biochemical Corp., U.S. Biochemical Amersham, Cleveland, OH). Suitable reporter molecules or labels which may be used include radionucleotides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

B7-related polynucleotide sequences, or fragments, or complementary sequences thereof, can be used in Southern or Northern analysis, dot blot, or other membrane-based technologies; in PCR

technologies; or in dip stick, pin, ELISA or biochip assays utilizing fluids or tissues from patient biopsies to detect the status of, e.g., levels or overexpression of BSL2, or to detect altered BSL2 expression. Such qualitative or quantitative methods are well known in the art (G.H. Keller and M.M. Manak (1993) *DNA Probes*, 2nd Ed, Macmillan Publishers Ltd., England; D.W. Dieffenbach and G. S. Dveksler (1995) *PCR Primer: A Laboratory Manual*, Cold Spring Harbor Press, Plainview, NY; B.D. Hames and S.J. Higgins (1985) *Gene Probes 1, 2,* IRL Press at Oxford University Press, Oxford, England).

BSL2 oligonucleotides may be chemically synthesized, generated enzymatically, or produced from a recombinant source. Oligomers will preferably comprise two nucleotide sequences, one with a sense orientation (5' → 3') and another with an antisense orientation (3' → 5'), employed under optimized conditions for identification of a specific gene or condition. The same two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers may be employed under less stringent conditions for detection and/or quantification of closely related DNA or RNA sequences.

Methods suitable for quantifying the expression of B7-related factors include radiolabeling or biotinylating nucleotides, co-amplification of a control nucleic acid, and standard curves onto which the experimental results are interpolated (P.C. Melby et al. (1993) *J. Immunol. Methods* **159**:235-244; and C. Duplaa et al. (1993) *Anal. Biochem.* 229-236). The speed of quantifying multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantification.

In a particular aspect, a nucleic acid sequence complementary to a B7-related polynucleotide, or fragment thereof, may be useful in assays that detect diseases relating to aberrant immune responses, particularly those described herein. A BSL2 polynucleotide can be labeled by standard methods, and added to a biological sample from a subject under conditions suitable for the formation of hybridization complexes. After a suitable

incubation period, the sample can be washed and the signal is quantified and compared with a standard value. If the amount of signal in the test sample is significantly altered from that of a comparable negative control (normal) sample, the altered levels of BSL2 nucleotide sequence can be correlated with the presence of the associated disease. Such assays may also be used to evaluate the efficacy of a particular prophylactic or therapeutic regimen in animal studies, in clinical trials, or for an individual patient.

To provide a basis for the diagnosis of a disease associated with altered expression of one or more B7-related factors, a normal or standard profile for expression is established. This may be accomplished by incubating biological samples taken from normal subjects, either animal or human, with a sequence complementary to a BSL2 polynucleotide, or a fragment thereof, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with those from an experiment where a known amount of a substantially purified polynucleotide is used. Standard values obtained from normal samples may be compared with values obtained from samples from patients who are symptomatic for the disease. Deviation between standard and subject (patient) values is used to establish the presence of the condition.

Once the disease is diagnosed and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to evaluate whether the level of expression in the patient begins to approximate that which is observed in a normal individual. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to diseases involving a hyperactive or hypoactive immune response, the presence of an abnormal levels (decreased or increased) of B7-related transcript in a biological sample (e.g., body fluid, cells, tissues, or cell or tissue extracts) from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to

employ preventative measures or aggressive treatment earlier, thereby preventing the development or further progression of the disease.

In one particular aspect, BSL2 oligonucleotides may be used for PCR-based diagnostics. For example, PCR can be used to perform Genetic Bit Analysis (GBA) of BSL2 in accordance with published methods (T.T. Nikiforov et al. (1994) *Nucleic Acids Res.* **22**(20):4167-75; T.T. Nikiforov et al. (1994) *PCR Methods Appl.* **3**(5):285-91). In PCR-based GBA, specific fragments of genomic DNA containing the polymorphic site(s) are first amplified by PCR using one unmodified and one phosphorothioate-modified primer. The double-stranded PCR product is rendered single-stranded and then hybridized to immobilized oligonucleotide primer in wells of a multi-well plate. Notably, the primer is designed to anneal immediately adjacent to the polymorphic site of interest. The 3' end of the primer is extended using a mixture of individually labeled dideoxynucleoside triphosphates. The label on the extended base is then determined. Preferably, GBA is performed using semi-automated ELISA or biochip formats (see, e.g., S.R. Head et al. (1997) *Nucleic Acids Res.* **25**(24):5065-71; T.T. Nikiforov et al. (1994) *Nucleic Acids Res.* **22**(20):4167-75).

In another embodiment of the present invention, oligonucleotides, or longer fragments derived from at least one B7-related polynucleotide sequence described herein may be used as targets in a microarray (e.g., biochip) system. The microarray can be used to monitor the expression level of large numbers of genes simultaneously (to produce a transcript image), and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disease, to diagnose disease, and to develop and monitor the activities of therapeutic or prophylactic agents. Preparation and use of microarrays have been described in WO 95/11995 to Chee et al.; D.J. Lockhart et al. (1996) *Nature Biotechnology* **14**:1675-1680; M. Schena et al. (1996) *Proc. Natl. Acad. Sci. USA* **93**:10614-10619; U.S. Patent No. 6,015,702 to P. Lal et al.; J. Worley et al. (2000) *Microarray Biochip Technology*, M. Schena, ed., Biotechniques Book, Natick, MA, pp.

65–86; Y.H. Rogers et al. (1999) *Anal. Biochem.* **266**(1):23-30; S.R. Head et al. (1999) *Mol. Cell. Probes.* **13**(2):81-7; S.J. Watson et al. (2000) *Biol. Psychiatry* **48**(12):1147-56.

In one application of the present invention, microarrays containing arrays of B7-related polynucleotide sequences can be used to measure the expression levels of B7-related factors in an individual. In particular, to diagnose an individual with a condition or disease correlated with altered BSL2 expression levels, a sample from a human or animal (containing, e.g., mRNA) can be used as a probe on a biochip containing an array of BSL2 polynucleotides (e.g., DNA) in decreasing concentrations (e.g., 1 ng, 0.1 ng, 0.01 ng, etc.). The test sample can be compared to samples from diseased and normal samples. Biochips can also be used to identify BSL2 mutations or polymorphisms in a population, including but not limited to, deletions, insertions, and mismatches. For example, mutations can be identified by: (i) placing B7-related polynucleotides of this invention onto a biochip; (ii) taking a test sample (containing, e.g., mRNA) and adding the sample to the biochip; (iii) determining if the test samples hybridize to the B7-related polynucleotides attached to the chip under various hybridization conditions (see, e.g., V.R. Chechetkin et al. (2000) *J. Biomol. Struct. Dyn.* **18**(1):83-101). Alternatively microarray sequencing can be performed (see, e.g., E.P. Diamandis (2000) *Clin. Chem.* **46**(10):1523-5).

In another embodiment of this invention, a B7-related nucleic acid sequence, or a complementary sequence, or fragment thereof, can be used as probes which are useful for mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial PI constructions, or single chromosome cDNA libraries (see C.M. Price (1993) *Blood Rev.*, **7**:127-134 and by B.J. Trask (1991) *Trends Genet.* **7**:149-154).

In a further embodiment of the present invention, antibodies which specifically bind to a BSL2 polypeptide may be used for the diagnosis

of conditions or diseases characterized by underexpression or overexpression of a BSL2 polynucleotide or polypeptide, or in assays to monitor patients being treated with a BSL2 polypeptide, peptide, or fusion protein, or a BSL2 agonist, antagonist, or inhibitor. The antibodies useful for diagnostic purposes may be prepared in the same manner as those for use in therapeutic methods, described herein. Diagnostic assays for a BSL2 polypeptide include methods that utilize the antibody and a label to detect the protein in biological samples (e.g., human body fluids, cells, tissues, or extracts of cells or tissues). The antibodies may be used with or without modification, and may be labeled by joining them, either covalently or non-covalently, with a reporter molecule. A wide variety of reporter molecules that are known in the art may be used, several of which are described herein.

A number of fluorescent materials are known and can be utilized to label a B7-related polypeptide or antibodies that specifically bind thereto. These include, for example, fluorescein, rhodamine, auramine, Texas Red, AMCA blue and Lucifer Yellow. A particular detecting material is anti-rabbit antibody prepared in goats and conjugated with fluorescein through an isothiocyanate. B7-related polypeptides or antibodies thereto can also be labeled with a radioactive element or with an enzyme. The radioactive label can be detected by any of the currently available counting procedures. Preferred isotopes include ^{3}H, ^{14}C, ^{32}P, ^{35}S, ^{36}Cl, ^{51}Cr, ^{57}Co, ^{58}Co, ^{59}Fe, ^{90}Y, ^{125}I, ^{131}I, and ^{186}Re. Enzyme labels are likewise useful, and can be detected by any of the presently utilized calorimetric, spectrophotometric, fluorospectrophotometric, amperometric, or gasometric techniques. The enzyme can be conjugated by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde, and the like. Many enzymes, which can be used in these procedures, are known and can be utilized. Preferred are peroxidase, β-glucuronidase, β-D-glucosidase, β-D-galactosidase, urease, glucose oxidase plus peroxidase, and alkaline phosphatase (see, e.g., U.S. Pat. Nos. 3,654,090; 3,850,752; and 4,016,043).

Antibody-based diagnostics and their application are familiar to those skilled in the art and may be used in accordance with the present

invention. As non-limiting examples, "competitive" (U.S. Pat. Nos. 3,654,090 and 3,850,752), "sandwich" (U.S. Pat. No. 4,016,043), and "double antibody," or "DASP" assays may be used. Several procedures including ELISA, RIA, and FACS for measuring B7-related polypeptide levels are known in the art and provide a basis for diagnosing altered or abnormal levels of B7-related polypeptide expression. Normal or standard values for B7-related polypeptide expression are established by incubating biological samples taken from normal subjects, preferably human, with antibody to the B7-related polypeptide under conditions suitable for complex formation. The amount of standard complex formation may be quantified by various methods; photometric means are preferred. Levels of the B7-related polypeptide expressed in the subject sample, negative control (normal) sample, and positive control (disease) sample are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another of its aspects, this invention relates to diagnostic kits for detecting B7-related polynucleotide(s) or polypeptide(s) as it relates to a disease or susceptibility to a disease, particularly the disorders of the immune system described herein. Such kits comprise one or more of the following: (a) a B7-related polynucleotide, preferably the nucleotide sequence of BSL2 (e.g., **SEQ ID NO:1**, 2, 4, or 6), or a fragment thereof; or (b) a nucleotide sequence complementary to that of (a); or (c) a B7-related polypeptide, preferably the polypeptide of BSL2 (e.g., **SEQ ID NO:3**, 5, or 7), or a fragment thereof; or (d) an antibody to a B7-related polypeptide, preferably to the polypeptide of BSL2 (e.g., **SEQ ID NO:3**, 5, or 7), or an antibody bindable fragment thereof. It will be appreciated that in any such kits, (a), (b), (c), or (d) may comprise a substantial component and that instructions for use can be included. The kits may also contain peripheral reagents such as buffers, stabilizers, etc.

The present invention also includes a test kit for genetic screening that can be utilized to identify mutations in B7-related factors. By identifying patients with mutated BSL2, and/or BSL2 DNA and comparing the

mutation to a database that contains known mutations in BSL2, and a particular condition or disease, identification and/or confirmation of, a particular condition or disease can be made. Accordingly, such a kit would comprise a PCR-based test that would involve transcribing the patients mRNA with a specific primer, and amplifying the resulting cDNA using another set of primers. The amplified product would be detectable by gel electrophoresis and could be compared with known standards for BSL2. Preferably, this kit would utilize a patient's blood, serum, or saliva sample, and the DNA would be extracted using standard techniques. Primers flanking a known mutation would then be used to amplify a fragment of BSL2. The amplified piece would then be sequenced to determine the presence of a mutation.

Therapeutics

Pharmaceutical compositions: The present invention contemplates compositions comprising a B7-related nucleic acid, polypeptide, fusion protein, antibody, ligand, modulator (e.g., agonist, antagonist, or inhibitor), or fragments or functional variants thereof, and a physiologically acceptable carrier, excipient, or diluent as described in detail herein. The present invention further contemplates pharmaceutical compositions useful in practicing the therapeutic methods of this invention. Preferably, a pharmaceutical composition includes, in admixture, a pharmaceutically acceptable excipient (carrier) and one or more of a B7-related polypeptide, fusion protein, nucleic acid, ligand, modulator, antibody, or fragment or functional equivalent thereof, as described herein, as an active ingredient. Because B7-related polypeptides or peptides are naturally occurring cellular components, they may be administered to an individual's circulatory system with minimal risk of undesired immunological complications.

The preparation of pharmaceutical compositions that contain biological reagents as active ingredients is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions, however, solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified. The active therapeutic ingredient is often mixed with

excipients that are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH-buffering agents, which enhance the effectiveness of the active ingredient.

Pharmaceutical compositions can be produced and employed in treatment protocols according to established methods depending on the disorder or disease to be treated (see, for example, P.D. Mayne (1996) *Cilnical Chemistry in Diagnosis and Treatment*, 6th ed., Oxford University Press, Oxford, England; Gilman et al., Eds. (1990) *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*, 8th ed., Pergamon Press; Avis et al., Eds. (1993) *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York, NY; and Lieberman et al., Eds. (1990) *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York, NY).

Pharmaceutical compositions may be produced as neutral or salt forms. Salts can be formed with many acids, including, but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic and succinic acids. Compositions can take the form of solutions, suspensions, suppositories, tablets, pills, capsules, sustained release compounds, or powders. Such formulations can contain 10%-95% (w/w) of the active ingredient, preferably 25%-70% (w/w). If the active compound is administered by injection, for example, about 1 µg-3 mg and preferably from about 20 µg-500 µg of active compound (e.g., B7-related fusion protein or antibody) per dosage unit may be administered. Pharmaceutical preparations and compositions can also contain one or more physiologically acceptable carrier(s), excipient(s), diluent(s), disintegrant(s), lubricant(s), plasticizer(s), filler(s), colorant(s), dosage vehicle(s), absorption enhancer(s), stabilizer(s), or bacteriocide(s). The production and formulation of such compositions and preparations are carried out by methods known and practiced in the art.

Exemplary formulations are given below:

Intravenous Formulation I:

Ingredient	mg/ml
BSL2 MAb	5.0
dextrose USP	45.0
sodium bisulfite USP	3.2
edetate disodium USP	0.1
water for injection q.s.a.d.	1.0 ml

Intravenous Formulation II:

Ingredient	mg/ml
BSL2 MAb	5.0
sodium bisulfite USP	3.2
disodium edetate USP	0.1
water for injection q.s.a.d.	1.0 ml

Intravenous Formulation III

Ingredient	mg/ml
BSL2 protein, Ig-fusion protein, or agonist	10.0
sodium bisulfite USP	3.2
disodium edetate USP	0.1
water for injection q.s.a.d.	1.0 ml

Intravenous Formulation IV

Ingredient	mg/ml
BSL2 protein, Ig-fusion protein, or agonist	10.0
dextrose USP	45.0
sodium bisulfite USP	3.2
edetate disodium USP	0.1
water for injection q.s.a.d.	1.0 ml

As used herein, "pg" means picogram, "ng" means nanogram, "μg" mean microgram, "mg" means milligram, "μl" mean microliter, "ml" means milliliter, and "l" means liter.

Following the preparation of pharmaceutical compositions, they may be placed in appropriate containers and labeled for the treatment of

indicated conditions. Such labeling can include amount, frequency, and method of administration. Preparations may be administered systemically by oral or parenteral routes. Non-limiting parenteral routes of administration include subcutaneous, intramuscular, intraperitoneal, intravenous, transdermal, inhalation, intranasal, intra-arterial, intrathecal, enteral, sublingual, or rectal administration.

A therapeutically effective amount of a pharmaceutical composition containing one or more B7-related polypeptides, fusion proteins, peptide fragments, or antibodies that specifically react with these components is an amount sufficient to reduce, ameliorate, or eliminate a disease or disorder related to altered activation levels of immune or inflammatory response cells, such as T-cells. An effective amount can be introduced in one administration or over repeated administrations to an individual being treated. Therapeutic administration can be followed by prophylactic administration, after treatment of the disease. A prophylactically effective amount is an amount effective to prevent disease and will depend upon the specific illness and subject. The therapeutically effective dose may be estimated initially, for example, either in cell culture assays or in animal models, usually mice, rats, rabbits, dogs, sheep, goats, pigs, or non-human primates. The animal model may also be used to determine the maximum tolerated dose and appropriate route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

Administration of the therapeutic compositions of the present invention to a subject can be carried out using known procedures, at dosages and for periods of time effective to achieve the desired result. For example, a therapeutically active amount of B7-related polypeptides, fusion proteins, peptides, or antibodies that react with these components may vary according to factors such as the age, sex, and weight of the individual, and the ability of the treatment to elicit a desired response in the individual. Dosages may be adjusted to provide the optimum therapeutic response. For example, several sequential doses may be administered daily or the dose may be proportionally reduced as indicated by the exigencies of the therapeutic situation.

Gene transfer therapy: In addition, host cells that are genetically engineered to carry the gene encoding a B7-related polypeptide, fusion protein, or peptide fragment comprising a fragment of a BSL2 polypeptide sequence (e.g., **SEQ ID NO:**3, 5, or 7), can be introduced into an individual in need of immunomodulation. Following expression and production of the B7-related polypeptide or peptide by the host cell, the so-produced B7-related polypeptide, fusion protein, or peptide can act to bind CD28/CTLA-4 and/or CD28-/CTLA-4-related ligand(s) to modulate the activation of immune or inflammatory response cells (e.g., T-cells) in the recipient. Host cells may be genetically engineered by a variety of molecular techniques and methods known to those having skill in the art, for example, transfection, infection, or transduction. Transduction as used herein commonly refers to cells that have been genetically engineered to contain a foreign or heterologous gene via the introduction of a viral or non-viral vector into the cells. Transfection more commonly refers to cells that have been genetically engineered to contain a foreign gene harbored in a plasmid, or non-viral vector. Host cells can be transfected or transduced by different vectors and thus can serve as gene delivery vehicles to transfer the expressed products into muscle.

Although viral vectors are preferred for gene transfer therapies, cells can be genetically engineered to contain nucleic acid sequences encoding the desired gene product(s) by various methods known in the art. For example, cells can be genetically engineered by fusion, transfection, lipofection mediated by the use of liposomes, electroporation, precipitation with DEAE-Dextran or calcium phosphate, particle bombardment (biolistics) with nucleic acid-coated particles (e.g., gold particles), microinjection, or genetically engineered microorganisms (K. Yazawa et al. (2000) *Cancer Gene Ther.* **7**:269-274). Vectors for introducing heterologous (i.e., foreign) nucleic acid (DNA or RNA) into muscle cells for the expression of active bioactive products are well known in the art. Such vectors possess a promoter sequence, preferably a promoter that is cell-specific and placed upstream of the sequence to be expressed. The vectors may also contain, optionally, one or more expressible marker genes for expression as an indication of

successful transfection and expression of the nucleic acid sequences contained in the vector. In addition, vectors can be optimized to minimize undesired immunogenicity and maximize long-term expression of the desired gene product(s) (see Nabel (1999) *Proc. Natl. Acad. Sci. USA* **96**:324-326). Moreover, vectors can be chosen based on cell-type that is targeted for treatment. For example, vectors for the treatment of tumor or cancer cells have been described (P.L. Hallenbeck et al. (1999) *Hum. Gene Ther.* **10**:1721-1733; T. Shibata et al. (2000) *Gene Ther.* **7**:493-498; M. Puhlmann et al. (2000) *Cancer Gene Ther.* **7**:66-73; N. Krauzewicz et al. (2000) *Adv. Exp. Med. Biol.* **465**:73-82).

Illustrative examples of vehicles or vector constructs for transfection or infection of the host cells include replication-defective viral vectors, DNA virus or RNA virus (retrovirus) vectors, such as adenovirus, herpes simplex virus and adeno-associated viral vectors. Adeno-associated virus vectors are single stranded and allow the efficient delivery of multiple copies of nucleic acid to the cell's nucleus. Preferred are adenovirus vectors. The vectors will normally be substantially free of any prokaryotic DNA and may comprise a number of different functional nucleic acid sequences. An example of such functional sequences may be a DNA region comprising transcriptional and translational initiation and termination regulatory sequences, including promoters (e.g., strong promoters, inducible promoters, and the like) and enhancers which are active in the host cells. Also included as part of the functional sequences is an open reading frame (polynucleotide sequence) encoding a protein of interest. Flanking sequences may also be included for site-directed integration. In some situations, the 5'-flanking sequence will allow homologous recombination, thus changing the nature of the transcriptional initiation region, so as to provide for inducible or noninducible transcription to increase or decrease the level of transcription, as an example.

In general, the encoded and expressed B7-related factor may be intracellular, i.e., retained in the cytoplasm, nucleus, or an organelle of a cell, or may be secreted by the cell. For secretion, the natural signal sequence

present in the B7-related structural gene may be retained. When the polypeptide or peptide is a fragment of a B7-related factor that is larger, a signal sequence may be provided so that, upon secretion and processing at the processing site, the desired protein will have the natural sequence. Specific examples of coding sequences of interest for use in accordance with the present invention include the BSL2 polypeptide coding sequences (e.g., **SEQ ID NO:**1, 2, 4, or 6). As previously mentioned, a marker may be present for selection of cells containing the vector construct. The marker may be an inducible or non-inducible gene and will generally allow for positive selection under induction, or without induction, respectively. Examples of marker genes include neomycin, dihydrofolate reductase, glutamine synthetase, and the like.

The vector employed will generally also include an origin of replication and other genes that are necessary for replication in the host cells, as routinely employed by those having skill in the art. As an example, the replication system comprising the origin of replication and any proteins associated with replication encoded by a particular virus may be included as part of the construct. The replication system must be selected so that the genes encoding products necessary for replication do not ultimately transform the cells. Such replication systems are represented by replication-defective adenovirus (see G. Acsadi et al. (1994) *Hum. Mol. Genet.* **3**:579-584) and by Epstein-Barr virus. Examples of replication defective vectors, particularly, retroviral vectors that are replication defective, are BAG, (see Price et al. (1987) *Proc. Natl. Acad. Sci. USA*, **84**:156; Sanes et al. (1986) *EMBO J.*, **5**:3133). It will be understood that the final gene construct may contain one or more genes of interest, for example, a gene encoding a bioactive metabolic molecule. In addition, cDNA, synthetically produced DNA or chromosomal DNA may be employed utilizing methods and protocols known and practiced by those having skill in the art.

According to one approach for gene therapy, a vector encoding a B7-related factor is directly injected into the recipient cells (*in vivo* gene therapy). Alternatively, cells from the intended recipients are explanted,

genetically modified to encode a B7-related factor, and reimplanted into the donor (*ex vivo* gene therapy). An *ex vivo* approach provides the advantage of efficient viral gene transfer, which is superior to *in vivo* gene transfer approaches. In accordance with ex vivo gene therapy, the host cells are first infected with engineered viral vectors containing at least one B7-related gene encoding a B7-related gene product, suspended in a physiologically acceptable carrier or excipient such as saline or phosphate buffered saline, and the like, and then administered to the host. The desired gene product is expressed by the injected cells, which thus introduce the gene product into the host. The introduced gene products can thereby be utilized to treat or ameliorate a disorder that is related to altered levels of the activation of immune or inflammatory response cells (e.g., T-cells).

Methods of immunomodulation: In accordance with the present invention, the BSL2 nucleic acid and polypeptide sequences can be used in the development of therapeutic reagents having the ability to either up-regulate (amplify) or down-regulate (suppress) immune responses (e.g., T-cell activation). In particular, B7-related polypeptides may interact with CD28 and thereby up-regulate immune cell activity. Alternatively, B7-related polypeptides may interact with CTLA-4 and thereby down-regulate immune cell activity. For example, soluble, dimeric forms of the B7-related polypeptides that bind to the CD28 and/or CD28-related ligand(s) but fail to provide a costimulatory signal to T-cells, can be used to block T-cell activation, and thereby provide a specific means by which to induce tolerance in a subject. Similarly, antibodies directed against one or more B7-related factors can be used to block the interaction between the B7-related factors and their cognate ligand(s), thereby preventing the activation of immune or inflammatory response cells (e.g., T-cells). In addition, fusion proteins comprising at least a fragment of a B7-related factor fused to at least the Fc domain of an IgG molecule can be used to up- or down-regulate cells expressing the cognate ligand(s) of the B7-related factor (e.g., T-cells). Furthermore, antisense or triplex oligonucleotides that bind to the nucleotide sequence of one or more B7-related factors can be used to decrease the

expression these factors. In contrast, cell surface, multivalent forms of B7-related factors that bind to CD28 and/or CD28-related ligand(s) and provide a costimulatory signal to immune or inflammatory response cells, such as T-cells, can be used to increase the activation of these cells. It is also possible to utilize more than one B7-related polypeptide, fusion protein, antibody, or therapeutically active fragments thereof, in order to up-regulate or down-regulate the activity of immune or inflammatory cells (e.g., T-cells) in an animal or human subject.

In addition, it may also be advantageous to employ B7-related therapeutics in conjunction with other therapeutics, surgeries, or treatments. For example, pharmaceutical compositions comprising BSL2vcvc-Ig or anti-BLS2 MAbs may be co-administered with one or more immunosuppressants including, but not limited to, corticosteroids such as cortisone, hydrocortisone (e.g., Cortef®), prednisone (e.g., Deltasone®, Meticorten®, or Orasone®), prednisolone (e.g., Delta-Cortef®, Pediapred®, or Prelone®), triamcinolone (e.g., Aristocort® or Kenacort®), methylprednisolone (e.g., Medrol®), dexamethasone (e.g., Decadron®, Dexone®, or Hexadrol®), and betamethasone (e.g., Celestone®); and other drugs including tacrolimus (e.g., Prograf® or FK506); azathioprine (e.g., Imuran); methotrexate (e.g., Rheumatrex®); glatiramer acetate (e.g., Copaxone®); cladribine (Leustatin); cyclophosphamide (e.g., Endoxan®, Cytoxan®, or Neosar®); Roquinimex (e.g., Linomide®); mitoxantrone (e.g., Novantrone®); mycophenolate mofetil (e.g., Cellcept®); cyclosporine (e.g., cyclosporin A; Sandimmune®); rapamycin (FRAP/mTOR inhibitor; sirolimus, e.g., Rapamune®); antithymocyte antibodies, for example, lymphocyte immune globulin (Atgam®), anti-Tac, and Rh(D) immune globulin (e.g., Rhogam or Gamulin); and similar drugs. In contrast, pharmaceutical compositions comprising other BSL2 polypeptides, fusion proteins, or antibodies may be co-administered with one or more immunostimulants, including, but not limited to, Bacille Calmette-Guérin (BCG), Levamisole, intravenous immune globulin (IVIG); cytokines such as interferon-α, interferon-γ, interferon-β-1b, IL-2 (e.g., recombinant human IL-2), G-CSF, and GM-CSF, and similar drugs.

Given the structure and function of the B7-related factors disclosed herein, it is possible to up-regulate or down-regulate the function of a B7-related factor in a number of ways. Down-regulating or preventing one or more B7-related factor functions (i.e., preventing high level lymphokine synthesis by activated T-cells) should be useful in treating autoimmune diseases, such as rheumatoid arthritis, multiple sclerosis, Lupus erythematosus, Hashimoto's thyroiditis, primary mixedema, Graves' disease, pernicious anemia, autoimmune atrophic gastritis, insulin dependent diabetes mellitus, good pasture's syndrome, myasthenia gravis, pemphigus, Crohn's disease, sympathetic opthalmia, autoimmune uveitis, autoimmune hemolytic anemis, idiopathic thrombocytopenia, primary biliary cirrhosis, ulcerative colitis, Sjogren's syndrome, polymyositis and mixed connective tissue disease. B7-related factors may also be down-regulated for the treatment of inflammation related to psoriasis, chronic obstructive pulmonary disease, asthma, and atherosclerosis. In addition, B7-related factors may be down-regulated for the treatment of tissue, bone marrow, and organ transplantation, and graft versus host disease. For example, blockage of T-cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated by its recognition as foreign material, followed by an immune reaction that destroys the transplant. The B7-related molecules of the present invention can also be used to treat or prevent cancers as described in detail below.

The B7-related nucleic acid molecules provided by the present invention can be used to design therapeutics to block the function of one or more B7-related factors. In particular, antisense or triplex oligonucleotides can be administered to prevent the expression of the BSL2 factors. For example, an oligonucleotide (e.g., DNA oligonucleotide) that hybridizes to a BSL2 mRNA can be used to target the mRNA for RnaseH digestion. Alternatively, an oligonucleotide that hybridizes to the translation initiation site of a BSL2 (e.g., **SEQ ID NO:**1, 2, 4, or 6) mRNA be used to prevent translation of the mRNA. In another approach, oligonucleotides that bind to the double-stranded DNA of the BSL2 gene(s) can be administered. Such

oligonucleotides can form a triplex construct and prevent the unwinding and transcription of the DNA encoding the targeted B7-related factor. In all cases, the appropriate oligonucleotide can be synthesized, formulated as a pharmaceutical composition, and administered to a subject. The synthesis and utilization of antisense and triplex oligonucleotides have been previously described (e.g., H. Simon et al. (1999) *Antisense Nucleic Acid Drug Dev.* **9**:527-31; F.X. Barre et al. (2000) *Proc. Natl. Acad. Sci. USA* **97**:3084-3088; R. Elez et al. (2000) *Biochem. Biophys. Res. Commun.* **269**:352-6; E.R. Sauter et al. (2000) *Clin. Cancer Res.* **6**:654-60).

In the context of this invention, antisense oligonucleotides are naturally-occurring oligonucleotide species or synthetic species formed from naturally-occurring subunits or their close homologues. Antisense oligonucleotides may also include moieties that function similarly to oligonucleotides, but have non-naturally-occurring portions. Thus, antisense oligonucleotides may have altered sugar moieties or inter-sugar linkages. Exemplary among these are phosphorothioate and other sulfur containing species which are known in the art.

In preferred embodiments, at least one of the phosphodiester bonds of the antisense oligonucleotide has been substituted with a structure that functions to enhance the ability of the compositions to penetrate into the region of cells where the RNA whose activity is to be modulated is located. It is preferred that such substitutions comprise phosphorothioate bonds, methyl phosphonate bonds, or short chain alkyl or cycloalkyl structures. In accordance with other preferred embodiments, the phosphodiester bonds are substituted with structures which are, at once, substantially non-ionic and non-chiral, or with structures which are chiral and enantiomerically specific. Persons of ordinary skill in the art will be able to select other linkages for use in the practice of the invention.

Antisense oligonucleotides may also include species that include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in nature may be so employed. Similarly, modifications on the furanosyl portions of the nucleotide subunits may also be

effected, as long as the essential tenets of this invention are adhered to. Examples of such modifications are 2'-O-alkyl- and 2'-halogen-substituted nucleotides. Some non-limiting examples of modifications at the 2' position of sugar moieties which are useful in the present invention include OH, SH, SCH_3, F, OCH_3, OCN, $O(CH_2)_n$ NH_2 and $O(CH_2)_n$ CH_3, where n is from 1 to about 10. Such antisense oligonucleotides are functionally interchangeable with natural oligonucleotides or synthesized oligonucleotides, which have one or more differences from the natural structure. All such analogs are comprehended by this invention so long as they function effectively to hybridize with BSL2 DNA or RNA to inhibit the function thereof.

For antisense therapeutics, the oligonucleotides in accordance with this invention preferably comprise from about 3 to about 50 subunits. It is more preferred that such oligonucleotides and analogs comprise from about 8 to about 25 subunits and still more preferred to have from about 12 to about 20 subunits. As defined herein, a "subunit" is a base and sugar combination suitably bound to adjacent subunits through phosphodiester or other bonds.

Antisense oligonulcleotides can be produced by standard techniques (see, e.g., Shewmaker et al., U.S. Patent No. 5,107,065). The oligonucleotides used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Equipment for such synthesis is available from several vendors, including PE Applied Biosystems (Foster City, CA). Any other means for such synthesis may also be employed, however, the actual synthesis of the oligonucleotides is well within the abilities of the practitioner. It is also will known to prepare other oligonucleotide such as phosphorothioates and alkylated derivatives.

The oligonucleotides of this invention are designed to be hybridizable with BSL2 RNA (e.g., mRNA) or DNA. For example, an oligonucleotide (e.g., DNA oligonucleotide) that hybridizes to B7-related mRNA can be used to target the mRNA for RnaseH digestion. Alternatively, an oligonucleotide that hybridizes to the translation initiation site of B7-related mRNA can be used to prevent translation of the mRNA. In another approach,

oligonucleotides that bind to the double-stranded DNA of BSL2 can be administered. Such oligonucleotides can form a triplex construct and inhibit the transcription of the DNA encoding BSL2 polypeptides. Triple helix pairing prevents the double helix from opening sufficiently to allow the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described (see, e.g., J.E. Gee et al. (1994) *Molecular and Immunologic Approaches*, Futura Publishing Co., Mt. Kisco, NY).

As non-limiting examples, antisense oligonucleotides may be targeted to hybridize to the following regions: mRNA cap region; translation initiation site; translational termination site; transcription initiation site; transcription termination site; polyadenylation signal; 3' untranslated region; 5' untranslated region; 5' coding region; mid coding region; and 3' coding region. Preferably, the complementary oligonucleotide is designed to hybridize to the most unique 5' sequence in BSL2, including any of about 15-35 nucleotides spanning the 5' coding sequence. Appropriate oligonucleotides can be designed using OLIGO software (Molecular Biology Insights, Inc., Cascade, CO).

In accordance with the present invention, the antisense oligonucleotide can be synthesized, formulated as a pharmaceutical composition, and administered to a subject. The synthesis and utilization of antisense and triplex oligonucleotides have been previously described (e.g., H. Simon et al. (1999) *Antisense Nucleic Acid Drug Dev.* **9**:527-31; F.X. Barre et al. (2000) *Proc. Natl. Acad. Sci. USA* **97**:3084-3088; R. Elez et al. (2000) *Biochem. Biophys. Res. Commun.* **269**:352-6; E.R. Sauter et al. (2000) *Clin. Cancer Res.* **6**:654-60). Alternatively, expression vectors derived from retroviruses, adenovirus, herpes or vaccinia viruses, or from various bacterial plasmids may be used for delivery of nucleotide sequences to the targeted organ, tissue or cell population. Methods which are well known to those skilled in the art can be used to construct recombinant vectors which will express nucleic acid sequence that is complementary to the nucleic acid sequence encoding a BSL2 polypeptide. These techniques are described

both in Sambrook et al. (1989) and in Ausubel et al. (1992). For example, BSL2 expression can be inhibited by transforming a cell or tissue with an expression vector that expresses high levels of untranslatable sense or antisense sequences. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and even longer if appropriate replication elements included in the vector system.

Various assays may be used to test the ability of specific antisense oligonucleotides to inhibit BSL2 expression. For example, mRNA levels can be assessed Northern blot analysis (Sambrook et al. (1989); Ausubel et al. (1992); J.C. Alwine et al. (1977) *Proc. Natl. Acad. Sci. USA* **74**:5350-5354; I.M. Bird (1998) *Methods Mol. Biol.* **105**:325-36), quantitative or semi-quantitative RT-PCR analysis (see, e.g., W.M. Freeman et al. (1999) *Biotechniques* **26**:112-122; Ren et al. (1998) *Mol. Brain Res.* **59**:256-63; J.M. Cale et al. (1998), *Methods Mol. Biol.* **105**:351-71), or *in situ* hybridization (reviewed by A.K. Raap (1998) *Mutat. Res.* **400**:287-298). Alternatively, antisense oligonucleotides may be assessed by measuring levels of BSL2 polypeptide, e.g., by western blot analysis, indirect immunofluorescence, immunoprecipitation techniques (see, e.g., J.M. Walker (1998) *Protein Protocols on CD-ROM*, Humana Press, Totowa, NJ).

The B7-related polypeptide sequences provided by the present invention may also be useful in the design of therapeutic agents to block or enhance the activity of immune response cells (e.g., T-cells). For example, a fusion protein comprising the soluble portion of a B7-related polypeptide conjugated with the Fc domain of human IgG can be constructed by standard recombinant techniques, described above. The BSL2-Ig (e.g., **SEQ ID NO:9**, 11, or 13) fusion proteins can be prepared as a pharmaceutical composition and administered to a subject. BSL2-Ig fusion proteins can be used to target specific T-cells for destruction, thereby reducing overall T-cell activation. Such treatment methods can be modeled on animal experiments, which utilize CTLA-4-Ig to prevent cardiac allograft rejection (Turka et al., *supra*). It will be

understood by a person skilled in the art that such methods may be adapted for use in humans, and for use with other conditions, including various transplants and autoimmune diseases. Alternatively, certain BSL2-Ig fusion proteins may be used to enhance T-cell activation.

As an alternative approach, antibodies that specifically react with B7-related polypeptides or peptides can be used to block the activity of immune or inflammatory response cells (e.g., T-cells). Antibodies or related antibody fragments that bind to peptides or polypeptides comprising the BSL2 (e.g., **SEQ ID NO:**3, 5, or 7) sequences can be formulated as pharmaceutical compositions and administered alone or in combination to a subject. Such antibodies can then inhibit the interaction of the B7-related polypeptides with CD28 and/or CD28-related ligands, and thereby prevent T-cell activation. Treatments utilizing antibodies directed against B7-related factors may be modeled on animal experiments, which use antibodies against CD28, B7-1, or B7-2 (D.J. Lenshow et al. (1995) Transplantation **60**:1171-1178; Y. Seko et al. (1998) *Circ. Res.* **83**:463-469; A. Haczku et al. (1999) *Am. J. Respir. Crit. Care Med.* **159**:1638-1643). One skilled in the art may adapt such methods for use in humans, and for use with various conditions involving inflammation or transplantation. It is noted that antibody-based therapeutics produced from non-human sources can cause an undesired immune response in human subjects. To minimize this problem, chimeric antibody derivatives can be produced. Chimeric antibodies combine a non-human animal variable region with a human constant region. Chimeric antibodies can be constructed according to methods known in the art (see Morrison et al. (1985) *Proc. Natl. Acad. Sci. USA* **81**:6851; Takeda et al. (1985) Nature **314**:452; U.S. Patent No. 4,816,567 of Cabilly et al.; U.S. Patent No. 4,816,397 of Boss et al.; European Patent Publication EP 171496; EP 0173494; United Kingdom Patent GB 2177096B). In addition, antibodies can be further "humanized" by any of the techniques known in the art, (e.g., Teng et al. (1983) *Proc. Natl. Acad. Sci. USA* **80**:7308-7312; Kozbor et al. (1983) *Immunology Today* **4**: 7279; Olsson et al. (1982) *Meth. Enzymol.* **92**:3-16; International Patent Application No. WO 92/06193; EP 0239400). Humanized antibodies can be

also be obtained from commercial sources (e.g., Scotgen Limited, Middlesex, Great Britain). Immunotherapy with a humanized antibody may result in increased long-term effectiveness for the treatment of chronic disease situations or situations requiring repeated antibody treatments.

In yet another approach, an isolated ligand of a B7-related factor can be used to down-regulate the activity of immune or inflammatory response cells (e.g., T-cells). For example, a soluble fusion protein comprising a B7-related factor ligand can be produced, isolated, and used to produce a pharmaceutical composition in accordance with the methods described in detail herein. This pharmaceutical composition can then be administered to a subject to bind to one or more endogenous B7-related factor(s) and block the activation of immune or inflammatory response cells (e.g., T-cells) as previously described.

Up-regulation of a B7-related factor function may also be useful in therapy. Because viral infections are cleared primarily by cytotoxic T-cells, an increase in cytotoxic activity would be therapeutically useful in situations where more rapid or thorough clearance of an infective viral agent would be beneficial to an animal or human subject. Notably, B7-1 acts to increase the cytotoxicity of T-cells though interactions with its cognate ligand(s). Thus, soluble active forms of B7-related polypeptides can be administered for the treatment of local or systemic viral infections, such as immunodeficiency (e.g., HIV), papilloma (e.g., HPV), herpes (e.g., HSV), encephalitis, influenza (e.g., human influenza virus A), and common cold (e.g., human rhinovirus) viral infections. For example, pharmaceutical formulations of active multivalent B7-related factors can be administered topically to treat viral skin diseases such as herpes lesions or shingles, or genital warts. Alternatively, pharmaceutical compositions of active, multivalent B7-related factors can be administered systemically to treat systemic viral diseases such as AIDS, influenza, the common cold, or encephalitis.

In addition, modulation of B7-related factor function may be useful in the induction of tumor immunity. For example, tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, or carcinoma

cells) can be genetically engineered to carry a nucleic acid encoding at least a fragment of at least one B7-related factor, such as BSL2 (e.g., **SEQ ID NO:**3, 5, or 7), and then administered to a subject to traverse tumor-specific tolerance in the subject. Notably, ectopic expression of B7-1 in B7 negative murine tumor cells has been shown to induce T-cell mediated specific immunity accompanied by tumor rejection and prolonged protection to tumor challenge in mice (L. Chen et al., *supra*; S. Townsend et al., *supra*; S. Baskar et al., *supra*). Tumor or cancer cell gene therapy treatments utilizing B7-related factors may be modeled on animal experiments (see K. Dunussi-Joannopoulos et al. (1997) *J. Pediatr. Hematol. Oncol.* **19**:356-340; K. Hiroishi et al. (1999) *Gene Ther.* **6**:1988-1994; B.K. Martin et al. (1999) *J. Immunol.* **162**:6663-6670; M. Kuiper et al. (2000) *Adv. Exp. Med. Biol.* **465**:381-390), or human phase I trial experiments (H.L. Kaufman et al. (2000) *Hum. Gene Ther.* **11**:1065-1082), which use B7-1 or B7-2 for gene transfer therapy. It will be understood that such methods may be adapted for use with various tumor or cancer cells. Additionally, tumor immunity may be achieved by administration of a B7-related fusion protein that directly stimulates the immune cells (see e.g., International Patent Application No. WO 01/21796 to V. Ling et al.).

The experiments described herein indicate that BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein can be used alone or in conjunction with one or more anti-BSL2 MAbs for therapeutic applications. BSL2vcvc ligand(s) and MAbs against BSL2 ligand(s) may also be useful as therapeutics. In particular, BSL2vcvc-Ig fusion protein (e.g., **SEQ ID NO:**9) can be used to inhibit disease progression in any disease where excessive or inappropriate activation of T-cells plays an important role. Such diseases would include, for example, acute and chronic transplant rejection, rheumatoid arthritis, multiple sclerosis, psoriasis, or other diseases described in detail herein. In addition, BSL2vcvc-Ig may also be used for specific applications such as xenotransplantation.

The experiments described herein demonstrate that anti-BSL2 MAbs (e.g., anti-BSL2-1 MAb, anti-BSL2-2 MAb, anti-BSL2-3 MAb, anti-BLS2-4 MAb, and anti-BSL2-5 MAb) function synergistically with BSL2-

4616811-Ig (BSL2vcvc-Ig) to inhibit T-cell proliferation. This indicates that anti-BSL2 MAbs may be used alone as therapeutics, if endogenous BSL2vcvc is expressed in sufficient amount by the subject's cells. If insufficient endogenous BSL2vcvc is expressed, co-administration of anti BSL2 MAbs with BSL2vcvc-Ig may be more effective than administration of either alone. In certain cases, however, it may be desirable to administer either BSL2-4616811-Ig (BSL2vcvc-Ig) or anti-BSL2 MAbs separately.

It may also be possible to engineer a bi-specific monoclonal antibody that could bring together endogenous BSL2vcvc and endogenous BSL2vcvc ligand on T-cells. The bi-specific antibody may thereby mimic the effect of co-administration of BSL2-4616811-Ig (BSL2vcvc-Ig) and one or more anti-BSL2 MAbs. In addition, signaling MAbs raised against BSL2vcvc ligand may be used to mimic the effect of BSL2vcvc-Ig, whereas blocking MAbs raised against BSL2vcvc ligand may act as immunostimulatory factors. It is also possible that soluble BSL2vcvc ligand may be used as an immunostimulatory factor.

EXAMPLES

The examples as set forth herein are meant to exemplify the various aspects of the present invention and are not intended to limit the invention in any way.

EXAMPLE 1: Database searches to identify BSL2

BSL2 was identified by BLAST and FASTA analysis of the Incyte Genomics sequence databases (Incyte Genomics) utilizing the B7-1 or B7-2 amino acid sequences as query sequences. For BLAST analysis, the BLOSSUM-62 scoring matrix was used (S. Henikoff et al. (1992) *Proc. Natl. Acad. Sci. USA* **89**:10915-10919), and the remaining parameters were set to the default designations. For FASTA analysis, all the parameters were set to the default designations (W.R. Pearson et al. (1988) *Proc. Natl. Acad. Sci. USA* **85**:2444-2448). The sequence database searches identified two Incyte Genomics 'templates': 252899.6 and the potential splice variant 252899.8. It is noted that Incyte Genomics templates are consensus EST sequences that are considered to represent mRNA transcripts.

Incyte Genomics template 252899.8 was used to identify Incyte Genomics clone 4616811. Incyte Genomics clone 4616811 belonged to Incyte Genomics Library ID No. BRAYDIT01, which was originally constructed using poly(A)$^+$ RNA from diseased hypothalamus tissue. Incyte Genomics clone 4616811 was obtained from Incyte Genomics and used for sequence analysis (ABI cycle sequencer, PE Biosystems) with the primers shown in **Table 1.**

TABLE 1

Clone	Primer	Sequence	**SEQ ID NO:**
4616811	392.423	ggtgcacagctttgctga	17
4616811	392.415	gctgtgcaccagctgttt	18
4616811	392.439	gctatgaaaggtccagag	19
4616811	392.499	gaatctggtggtgtccaa	20
4616811	392.1716	ctctgtcaccatcacagg	21
4616811	392.852	ctctgtcaccatcacacc	22
4616811	392.523	gaaatcccggatgctcac	23
4616811	392.766A	accacacgtgttccagca	24
4616811	392.766B	tgctggaacacgtgtggt	25
4616811	392.383	ggccctcagcaaagctgt	26
4616811	392.1448	agctgtaggtgccattcg	27
4616811	392.892	agggacctggacctccac	28
4616811	392.1528	tgggggggaatgtcatagg	29
4616811	392.1215	agcaggcaggatgactta	30
4616811	392.1242	aacagaccacccacaacc	31
6487516	314.570	gcaaatggcacctacagc	32
6487516	314.634	tctggggtgtgatggtga	33
6487516	314.450	atgaaaggtccagagggc	34
6487516	314.584	acccataattcttaccca	35
6487516	314.824	cacagctctgtttgatct	36
6487516	314.644	ctcctaccctctggctgc	37

Notably, the predicted amino acid sequence of Incyte Genomics clone 4616811 contained 2 sets of v/c (variable/constant domain) folds, whereas typical B7-related amino acid sequences contain only 1 set of v/c folds. Seqweb Gap (Genetics Computer Group) analysis indicated that the BSL2-4616811 sequence shared less than 50% sequence identity with B7-1, B7-2, B7-H1 nucleotide sequences, while the BSL2-4616811 amino acid sequence shared less than 35% sequence identity with the B7-1, B7-2, and B7-H1 amino acid sequences. A sequence similar to BSL2-4616811 has also been identified as an amyloid precursor protease in International Patent

Application No. WO 00/68266 to G.W. Becker et al.

The nucleotide and predicted amino acid sequences of Incyte Genomics clone 4616811 (BSL2-4616811) are shown in **Figures 1A-1C**. The plasmid carrying DNA encoding BSL2-4616811 (pINCY:BSL2-4616811) was deposited with the American Type Culture Collection (ATCC, 10801 University Blvd., Manassas, VA 20110-2209 USA) in accordance with the Budapest Treaty, under ATCC Designation No. PTA-1993, on June 6, 2000.

EXAMPLE 2: Full-length cloning of the BSL2

To verify the sequence of Incyte Genomics clone 4616811, PCR primers were designed to amplify the nucleotide sequence from the predicted translation start codon to the predicted translation stop codon of the clone: forward primer BSL2-7 (5'-atgctgcgtcggcg-3'; **SEQ ID NO:38**); reverse primer BSL2-8 (5'-tcaggctatttcttgtccatcatc-3'; **SEQ ID NO:39**).

A HMVEC library was constructed utilizing the SMART™ RACE cDNA Amplification Kit (CLONTECH) according to manufacturer's instructions, using poly(A)$^+$ RNA obtained from human microvascular endothelial cells treated with TNF-alpha for 1 hr as the RACE reaction template. The PCR mixture included 1 µl PCR-ready HMVEC library, 5 µl PCR buffer (GibcoBRL), 1.5 µl 50 mM $MgCl_2$, 1 µl 10 mM dNTPs (Boehringer Mannheim Biochemicals/Roche Molecular Biochemicals, Indianapolis, IN), 25 pMol BSL2-7 primer, 25 pMol BSL2-8 primer, and 1 µl CLONTECH Advantage Enzyme mix in a total volume of 50 µl. PCR was performed in a PE Biosystems Thermal Cycler model 9700. The PCR mixture was incubated at 94°C for 1 min, followed by 35 cycles of incubation at 94°C for 30 sec, 60°C for 30 sec, and 72°C for 45 sec, followed by incubation at 72°C for 10 min.

One microliter of the PCR mixture was ligated directly into pCR2.1 (Invitrogen) according to the manufacturer's directions. One half of the ligation mixture was used for transformation into Max-Efficiency DH5-alpha *E coli* cells (GibcoBRL) in accordance with the manufacturer's directions. Transformants were plated onto LB agar plates with 100 µg/ml ampicillin and 30 µg/ml X-gal and incubated at 37°C overnight. White colonies were isolated and grown overnight at 37°C in 5 ml LB broth

containing 100 μg/ml ampicillin.

Plasmid DNA was isolated from the bacterial culture using Spin Miniprep kit (QIAGEN) according to the manufacturer's directions. DNA was digested with *Eco*RI to release the cloned insert, and the digestion mixture was analyzed by electrophoresis on a 1% agarose gel. Insert fragments larger than 700-bp were sequenced using the vector-specific M13 (5'-gttttcccagtcacgac-3'; **SEQ ID NO:**40) and M13 reverse (5'-caggaaacagctatgac-3'; **SEQ ID NO:**41) sequencing primers (ABI cycle sequencer, PE Applied Biosystems).

Sequence analysis indicated that two splice variants of BSL2 had been cloned: BSL2-L165-21 and BSL2-L165-35b. The BSL2-L165-21 and BSL2-L165-35b splice variants encoded amino acid sequences that each contained one v/c fold and were ~95% identical to one another. Seqweb Gap analysis (Genetics Computer Group) also indicated that the BSL2-L165-21 and BSL2-L165-35b nucleotide sequences shared less than 50% sequence identity with B7-1, B7-2, and B7-H1 nucleotide sequences, while the BSL2-L165-21 and BSL2-L165-35b amino acid sequences shared less than 35% sequence identity with the B7-1, B7-2, and B7-H1 amino acid sequences.

Sequence analysis further indicated that the amino acid and nucleotide sequences of BSL2-L165-21 shared less than 99% sequence identity with the PRO352 amino acid and nucleotide sequences, respectively, reported in International Patent Application No. WO 99/46281 to K.P. Baker et al. The amino acid and nucleotide sequences of BSL2-L165-35b shared less than 99.5% sequence identity with the PRO352 amino acid and nucleotide sequences, respectively.

Amino acid sequence alignments using GCG Gap program (GCG, Madison, WI) indicated that the longest stretch of identical amino acid residues shared by BSL2-L165-21 and PRO352 was 88 contiguous amino acids in length. The longest stretch of identical amino acid residues shared by BSL2-L165-35b and PRO352 was 168 contiguous amino acids in length. Analysis with ClustalW (J.D. Thompson et al. (1994) *Nucleic Acids Res.* **22**:4673-4680 indicated that the longest stretch of identical amino acids

shared by BSL2-4616811 and PRO352 was 206 contiguous amino acids in length.

Nucleotide sequence alignments indicated that the longest stretch of identical bases shared by BSL2-L165-21 and PRO352 was 254 contiguous nucleotides in length. The longest stretch of identical bases shared by BSL2-L165-35b and PRO352 was 305 contiguous nucleotides in length. The longest stretch of identical bases shared by BSL2-4616811 and PRO352 was 618 contiguous nucleotides in length. Notably, BSL2-L165-35b has also been identified as B7-H3, a co-stimulatory molecule for T-cell activation (A.I. Chapoval et al. (2001) *Nature Immunology* **2**:269-274).

The nucleotide and predicted amino acid sequences of the BSL2-L165-21 splice variant are shown in **Figures 2A-2B**, while the nucleotide and predicted amino acid sequences of BSL2-L165-35b are shown in **Figures 3A-3B**. The plasmid carrying DNA encoding BSL2-L165-21 (pCR2.1:BSL2-L165-21) was deposited with the American Type Culture Collection (ATCC, 10801 University Blvd., Manassas, VA 20110-2209 USA) in accordance with the Budapest Treaty, under ATCC Designation No. PTA-1987, on June 6, 2000. In addition, the plasmid carrying DNA encoding BSL2-L165-35b (pCR2.1:BSL2-L165-35b) was deposited with the American Type Culture Collection (ATCC, 10801 University Blvd., Manassas, VA 20110-2209 USA) in accordance with the Budapest Treaty, under ATCC Designation No. PTA-1988, on June 6, 2000.

EXAMPLE 3: Northern Blotting to determine BSL2 expression analysis

BSL2 expression patterns were determined by Northern blot analysis of various tissue and cell types, using the BSL2-4616811-derived probe that binds to the various forms of BSL2 (e.g., BSL2vcvc, BSL2v2c2, and BSL2v1c2). For Northern blot analysis, 0.5 µg of total poly(A)$^+$ RNA obtained from each cell type was separated on a 1.2% agarose gel containing 3% formaldehyde, and transferred to a Hybond-N+ nylon membrane (Amersham) ovemight using 20 X SSC as transfer buffer. The membrane was then auto-crosslinked, washed with 4 X SSPE, and allowed to air-dry. The membrane was then prehybridized at 65°C in ExpressHyb solution

(CLONTECH) for 1 hr, and then hybridized with a [^{32}P]-dCTP-radiolabeled (NEN, Boston, MA) random primed BSL2 cDNA probe. The probe (**Figure 7A**) was purified using the NucTrap purification column (Stratagene), and radiolabeled to have a specific activity of 2.0 x 10^6 cpm/ml. Following hybridization, the membrane was washed in 2.0 X SSC with 0.05% SDS at 65°C, and exposed to film for 72 hr at -70°C.

A 3.6-kb BSL2 mRNA transcript was detected in several cell types. In particular, high levels of BSL2 mRNA were detected in all HMVEC stimulated with TNF-alpha. Moderate levels of BSL2 mRNA were detected in resting THP1 cells, and THP1 cells activated with LPS (**Figure 7B**). In contrast, low levels of BSL2 mRNA were detected in peripheral blood monocytes stimulated with PHA or GM-CSF/IL-4, and BSL2 mRNA was not detected in resting or stimulated peripheral blood T-cells, or in resting RAJI cells, resting RAMOS cells, or serum starved H292 cells (**Figure 7B**).

EXAMPLE 4: PCR assay to determine relative abundance of BSL2-4616811 (BSL2vcvc) and BSL2-L165-35b (BSL2v1c2)

To determine whether BSL2-4616811 (BSL2vcvc) or BSL2-L165-35b (BSL2v1c2) was predominant species of BSL2, and whether predominance corresponded with cell type and/or stimulus type, the following experimental approach was used. Analysis of the genomic sequence of BSL2 indicated that the sequence includes several exons separated by introns. It was presumed that a primary transcript was produced from this sequence, and the primary transcript was spliced to yield BSL2-4616811 mature RNA. Analysis of BSL2-4616811 sequence showed that it coded for the following: a 5' UTR, an initiating ATG, a signal peptide sequence, a variable Ig fold (v1), an Ig constant fold (c1), an Ig V fold (v2), an Ig C fold (c2), a short hinge a putative transmembrane domain, a short cytoplasmic tail, a stop codon, and a 3' UTR.

The BSL2-4616811 coding sequence appeared unique in the human genome, as the v1 and c1 (v1c1) sequence was about 95% identical to the v2 and c2 (v2c2) sequence at the amino acid level. Importantly, all of the structurally important residues were conserved in the v1c1 and v2c2

amino acid sequences, and most of the changes from v1c1 to v2c2 were conservative changes. A schematic of the BSL2-4616811 (BSL2vcvc), BSL2-L165-21 (BSL2v2c2), and BSL2-L165-35b (BSL2v1c2) v/c domains is show in **Figure 3C**.

Despite the 96% identity between v1c1 and v2c2 at the nucleotide level, sequence comparison between the two regions using GCG Gap revealed one short region of relatively low homology. A forward primer designated BSL2-9 was designed to take advantage of this short region of low homology. BSL2-9 was designed to bind specifically to v. **Figure 8E** demonstrates the specificity of the BSL2-9 primer. A reverse primer, BSL2-11 was designed to hybridize to the hinge sequence.

Notably, the BSL2-4616811 transcript contained both the BSL2-9 v1-binding site in v1 and the homologous site in v2. The BSL2-L165-35b transcript contained only the BSL2-9 v1 binding site. The BSL2-L165-21 transcript contained only the v2 site. Accordingly, PCR performed with primers BSL2-9 and BSL2-11 was expected to produce: 1) a PCR product of approximately 1150-bp, representing BSL2-4616811; or 2) a PCR product of about 550-bp, representing BSL2-L165-35b.

PCR was initially conducted with BSL2-4616811 plasmid to confirm the specificity of the BSL2-9 primer. PCR was performed using 2 µl of 10 ng/µl BSL2-4616811 plasmid DNA, 5 µl PCR buffer (GibcoBRL), 1.5 µl of 25 mM $MgCl_2$ (GibcoBRL), 1 µl of 10 mM dNTPs (GibcoBRL), 2.5 µl of 10 pMol/µl BSL2-9 primer (5' tggtgcacagctttgct 3'; **SEQ ID NO:**42), 2.5 µl of 10 pMol/µl BSL2-11 primer (5' tctgggggaatgtcat 3'; **SEQ ID NO:**43), 0.5 µl of 5 U/µl GibcoBRL platinum Taq DNA polymerase (Cat. # 10966-018), and 35 µl dH_2O. PCR was performed on a PE Biosystems 9700 using the following cycling conditions: 94°C for 30 sec; followed by 35 cycles of 94°C for 30 sec, 61°C for 30 sec, 72°C for 60 sec; followed by 72°C for 10 min. Following this, 40 µl of the PCR reaction was run on a 1.2% agarose gel next to Lambda *Bst*EII DNA ladder (New England Biolabs Beverly, MA; Cat. # 301-4S). The 1150-bp band was predominant, indicating that the BSL2-9 PCR primer was specific for the BSL2-4616811 sequence (**Figure 8E**).

RAJI, RAMOS, PM-LCL, PL-LCL, and CE-LCL B-like cell lines; HL-60 and Thp1 monocytic like cell lines; and CEM and Hut78 T-like cell lines were grown in RPMI 1640 with 10% FBS and 1% GibcoBRL penicillin/streptomycin to a concentration of 5 x 10^5 cells/ml. The cultures were split and one-half of the B-like and T-like cell cultures were stimulated with 30 ng/ml PMA and 1 μM ionomycin for 24 hr. Monocytic cell lines were stimulated with 1 μg/ml LPS for 24 hr. Early passage HUVEC were grown to 90% confluence, and one-half of the culture was stimulated with 10 ng/ml TNFα, and harvested at 6 or 24 hr. Unstimulated HUVEC were harvested at 24 hr. Peripheral blood T-cells from two donors were purified as described below.

Cells were added (1 x 10^6 cells/ml) to RPMI 1640 with 10% human serum and 1% GibcoBRL penicillin/streptomycin. Cells were then incubated at 37°C in 5% CO_2 for 72 hr. T75 flasks were coated with 1 μg/ml CD3 MAb G19.4 (described herein) in PBS for 4 hr at 37°C. The flask was washed twice with PBS, and cells were added (1 x 10^5 cells/ml) in RPMI 1640 with 10% human serum and 1% GibcoBRL penicillin/streptomycin. CD28 MAb 9.3 (described herein) was added to a final concentration of 1 μg/ml. Cells were grown at 37°C in 5% CO_2 for 72 hr. Cells were added (1 x 10^6 cells/ml) to RPMI 1640 with 10% human serum and 1% GibcoBRL penicillin/streptomycin. PMA was added to 30 ng/ml and ionomycin was added to 1 μM and incubated at 37°C in 5% CO_2 for 48 hr. Proliferation of stimulated T-cells was confirmed visually. All cell types were pelleted and frozen on dry ice and stored at - 70°C until use.

Total RNA was prepared using the Invitrogen (Carlsbad, CA) SNAP total RNA isolation kit (Cat. # K1950-01) according to the manufacturer's instructions. First strand cDNA was produced using the GibcoBRL Superscript First-Strand Synthesis System for RT-PCR (Cat. # 11904-018) according to the manufacturer's instructions for oligo dT priming. PCR was performed using 2 μl first strand cDNA, 5 μl PCR buffer (GibcoBRL), 1.5 μl of 25 mM $MgCl_2$ (GibcoBRL), 1 μl of 10 mM dNTPs (GibcoBRL), 2.5 μl of 10 pMol/μl BSL2-9 primer (5' tggtgcacagctttgct 3'; **SEQ ID NO**:44), 2.5 μl of

10 pMol/μl BSL2-11 primer (5' tctgggggaatgtcat 3'; **SEQ ID NO:**45), 0.5 μl of 5 U/μl GibcoBRL platinum Taq DNA polymerase (Cat. # 10966-018), and 35 μl dH_2O. PCR was performed on a PE Biosystems 9700 using the following cycling conditions: 94°C for 30 sec; followed by 35 cycles of 94°C for 30 sec, 61°C for 30 sec, 72°C for 60 sec; followed by 72°C for 10 min. Following this, 40 μl of the PCR reaction mixture was run on a 1.2% agarose gel.

PCR analysis indicated that certain cell types contained predominantly the BSL2-4616811 (BSL2vcvc) transcript, with or without stimulation. Unstimulated and stimulated PL-LCL cells showed higher levels of the BSL2-4616811 transcript than the than the BSL2-L165-35b transcript (**Figure 8A**). Both unstimulated and stimulated HUVEC cells showed higher levels of the BSL2-4616811 transcript than the BSL2-L165-35b transcript (**Figure 8B**).

In contrast, other cell types contained predominantly the BSL2-L165-35b (BSL2v1c2) transcript, with or without stimulation. Stimulated RAJI cells, and unstimulated and stimulated RAMOS cells showed higher levels of the BSL2-L165-35b transcript than the BSL2-4616811 transcript (**Figure 8A**). Unstimulated and stimulated HL60 cells showed higher levels of the BSL2-L165-35b transcript than the BSL2-4616811 transcript (**Figure 8B**).

In addition, certain cell types showed an increase in BSL2-4616811 (BSL2vcvc) transcript levels upon activation. Unstimulated PM-LCL cells showed higher levels of the BSL2-4616811 transcript, which increased relative to the BSL2-L165-35b transcript upon stimulation (**Figure 8A**). Similarly, unstimulated CE-LCL cells showed higher levels of the BSL2-4616811 transcript, which increased relative to the BSL2-L165-35b transcript upon stimulation (**Figure 8B**). Unstimulated Thp1 cells showed equivalent levels of the BSL2-4616811 and the BSL2-L165-35b transcript, however, levels of the BSL2-4616811 transcript increased upon stimulation (**Figure 8B**). Unstimulated peripheral blood T-cells from donor 079 showed predominantly BSL-L165-35b but shifted to predominantly BSL2-4616811 upon stimulation. Peripheral blood T-cells from donor 124 showed a less dramatic shift from BSL2-L165-35b to BSL2-4616811 upon stimulation

(**Figure 8C**). Unstimulated CEM cells showed higher levels of the BSL2-L165-35b transcript, but levels of the BSL2-4616811 transcript increased upon activation (**Figure 8D**).

Other cell types showed an increase in BSL2-L165-35b (BSL2v1c2) levels upon activation. Unstimulated HUT78 cells showed higher levels of the BSL2-4616811 transcript, but levels of the BSL2-L165-35b transcript increased upon activation (**Figure 8D**). These results, coupled with the conservation of the amino acid sequences in all four Ig folds, the conservation of structurally important amino acid residues in all four Ig folds, and the conservative nature of the amino acid differences between v1c1 and v2c2, support a function for BSL2-4616811 (BSL2vcvc) which is distinct from BSL2-L165-35b (BSL2v1c2) and BSL2-L165-21 (BSL2v2c2).

To rule out the presence of PCR artifacts, the PCR product from HUVEC activated with TNFα for 24 hr was cloned using the Invitrogen Original TA Cloning Kit (Cat. # K2000-01) according to the manufacturer's directions. The construct was used for transformation into bacterial cells, and 25 white colonies were isolated and grown in LB with 100 μg/ml ampicillin. DNA preps were made and sequencing was performed. Of the 25 clones, 10 clones did not contain insert, 3 clones did not produce readable sequence, 3 clones contained BSL2-related sequences with extensive deletions, and the remaining 9 clones produced sequence consistent with BSL2-4616811.

It was noted that no PCR product corresponding to BSL2-4616811 or BSL2-L165-35b was observed in unstimulated RAJI cells. To confirm this result, PCR was repeated for unstimulated and unstimulated RAJI cells as previously described. Again, no PCR product was detected for the unstimulated RAJI cells. Following this, PCR was performed using G3PDH primers with template isolated from unstimulated and stimulated RAJI cells. Cycling conditions were identical to those described above, except the annealing temperature was 55°C, and the extension time was 45 sec. Relatively equal amounts of G3PDH product was detected for both unstimulated and stimulated RAJI cells. This provided further support for the

observation that unstimulated RAJI cells do not contain detectable BSL2 transcript.

EXAMPLE 5: Purification of peripheral blood T-cells

Preparation of monocytes: Human monocytes were obtained from peripheral blood mononuclear cells by elutriation. The elutriation buffer contained 1 L RPMI (GibcoBRL/Life Technologies Inc., Rockville, MD; Cat. #11875-085) with 2.5 mM EDTA and 10 μg/ml polymyxin B. The buffer was prepared 1 day prior to the elutriation procedure, and stored at room temperature. For the elutriation procedure, 225 ml EDTA whole blood/donor was obtained and prepared. Twenty milliliters of elutriation buffer was added to twelve 50 ml centrifuge tubes, and the 225 ml of blood was divided equally among the tubes. Twelve milliliters of ficoll solution (lymphocyte separation medium) was used to underlay the mixture in each tube (AccuPrep Lymphocytes, Accurate Scientific Co.; Cat. # 1053980). The tubes were centrifuged at 1800 rpm for 25 min (minutes).

Sheep's red blood cells (SRBC) were prepared by the following procedure. Twelve milliliters of Sheep Blood Alsever's (Colorado Serum Co., Denver, CO; Cat. # CS1112) was resuspended, and centrifuged at 2000 rpm for 10 min. The top coating of the SRBC pellet was removed, and the pellet was washed 2 times with elutriation buffer. Following each wash, the pellet was centrifuged at 2200 rpm for 8 min. After the second wash, the pellet was resuspended in 5 ml elutriation buffer and refrigerated.

Following centrifugation, the supernatant from the ficoll underlay tubes was aspirated to leave behind approximately 5 ml of the interface layer. The interface layer was then carefully removed to a new tube, without disturbing the red cell pellet in each tube. The interface layers of two 50 ml tubes was combined and transferred to a new 50 ml tube, resulting in a total of six 50 ml tubes. Elutriation buffer was added to each tube to bring the final volume to 50 ml per tube. The tubes were centrifuged at 1800 rpm for 10 min, and the supernatant was removed. The peripheral blood monocytes from each donor were combined and divided between two tubes, and resuspended in 40 ml elutriation buffer per tube. The tubes were centrifuged at 1500 rpm

for 10 min, the supernatant was aspirated, and the pellet was resuspended in 30 ml elutriation buffer per tube.

Following this step, 3 ml of washed SRBC was added to each tube, and the mixture was centrifuged at 1000 rpm for 5 min. The pellet was incubated on ice for at least 1 hr (hour), and each pellet was gently resuspended by inverting the tubes. Twelve milliliters of ficoll was used to underlay the mixture in each tube. The tubes were centrifuged at 2500 rpm for 20 min, and the interface layers were removed to new tubes as previously described. The interface layers were then resuspended in 10 ml elutriation buffer and stored on ice until the start of the elutriation procedure. It is noted the purification of T-cells using their affinity to SRBCs is termed E-rosetting.

Elutriation of monocytes: Elutriation was performed as follows. The elutriation pump speed was set to ~65 ml/min, and the storage ethanol was removed from the feed lines for the pump. The feed lines, chambers, and rotor were washed with ~100 ml distilled water. Pump speed was reduced to 50 ml/min, and elutriation buffer was passed through the feed lines, chamber, and rotor. The feed lines were checked for the presence of bubbles, and any bubbles were removed. The centrifuge speed was then set at 1950 ± 1 rpm, and the pump was calibrated at 15 ml/min. The pump speed was then reduced to 11 ml/min and the stopcock to the chamber was closed.

To load cells, the loading syringe stopcock was closed and the outlet pipette was placed in the 50 ml sample tube labeled as 11 ml/min fraction. The cells were mixed and added to the loading syringe. The stopcock of the loading syringe was opened and the feeding tube was rinsed with 10 ml elutriation buffer. When ~ 0.5 ml cells remained in the syringe, elutriation buffer was added and this step was repeated one more time. Following this step, the loading syringe stopcock was closed and the chamber stopcock was opened.

Fifty milliliter fractions were collected at 11 (2 fractions), 14, 16, and 36 (2 fractions) ml/min pump speeds, and then placed on ice. In accordance with previous observations, the monocytes were predicted to be in the 36 ml/min fraction. The monocyte fraction was centrifuged at 1800 rpm

for 8 min, and the cells were resuspended in 10 ml 25% fetal bovine serum/RPMI with 1 µg/ml polymyxin B. The cells were counted and stored on ice until use.

Cell culture conditions: The isolated peripheral blood monocytes were resuspended in RPMI 1640 medium containing 10% fetal bovine serum (Hyclone, Logan, UT) supplemented with penicillin/streptomycin, 2 mM glutamine, 1% non-essential amino acids, 1 mM sodium pyruvate, and IL-4 (75 ng/ml) and GM-CSF (15 ng/ml) cytokines (each from GibcoBRL). The cell suspension (5 x 10^5 cells/ml) was transferred to tissue culture flasks and incubated in chambers containing 5% CO_2 at 37°C for 7 days. Following the incubation period, the cell cultures were pipetted vigorously to remove cells from the flask. The human monocytic cell line THP1 was grown at 37°C in 5% CO_2 to a final concentration of 5 x 10^5 cells/ml in RPMI 1640 medium containing 10% fetal bovine serum supplemented with penicillin/streptomycin and 2 mM glutamine.

EXAMPLE 6: BSL2-L165-35b-Ig (BSL2v1c2-Ig) fusion construct

BSL2-L165-35b-Ig (BSL2v1c2-Ig) was constructed as follows. The extracellular domain of BSL2-L165-35b was amplified by PCR from an L165-35b DNA preparation. The PCR reaction included 1 µl of a 1/1000 dilution of the L165-35b template, PCR buffer, dNTP, and $MgCl_2$ from Gibco (described herein), 2.5 µl of 10 µM primer BSL2-L165-21-Ig-1, 2.5 µl of 10 µM primer BSL2-L165-21-Ig-2 (both primers were described for the BSL2-4616811-Ig construction, below), and 1 µl CLONTECH AdvanTaq Plus (Palo Alto, CA; Cat. # 8431-1) in a total volume of 50 µl. PCR conditions included incubation at 94°C for 1 min; followed by 20 cycles of incubation at 94°C for 30 sec, 59°C for 30 sec, 72°C for 45 sec; followed by incubation at 72°C for 10 min. PCR was performed on a PE Applied Biosystems (Perkin-Elmer, Foster City, CA) GeneAmp PCR System 9700 thermal cycler.

Following PCR, 10 µl of the reaction mixture was run on a 1.2% agarose/0.5 X TBE gel to check for product. The remainder of the PCR reaction mixture was digested at 37°C with 20 U *Kpn*I (Roche Molecular, Indianapolis IN; Cat. # 899 186) and 20 U *Eco*RI (Roche Molecular, Cat. #

703 737) in a total volume of 80 µl for 16 hr. The digestion mixture was run on a 1.2% agarose/0.5% TBE gel. A predominant band of about 700-bp was purified using the QIAGEN Qiaquick Gel Extraction Kit (Valencia CA; Cat. # 28704). Following this, 5 µl of 50 µl recovered product was run on a 1.2% agarose/0.5% TBE gel and the DNA concentration was estimated as 10 ng/µl. Then, 15 ng recovered product was ligated into 30 ng of L200-1 (vector described herein) digested with *Kpn*I plus *Eco*RI using 5 U Gibco T4 DNA ligase (Cat. # 15224-041) in a total volume of 10 µl (ligation number L315). The reaction was incubated at 14°C for 3 hr.

One-half of the reaction mixture was used for transformation into Gibco MaxEfficiency DH5α competent *E coli* (Cat. # 18256-012). Transformants were plated on LB plates plus 100 µg/ml ampicillin and incubated at 37°C for 18 hr. Bacterial colonies were grown in 5 ml LB plus 100 µl/ml ampicillin for 16 hr. DNA preps were made using QIAGEN Qiaprep Spin Miniprep Kit (Cat. # 27106). Isolates L315-1 and L315-3 were determined by sequence analysis to be correct. The BSL2-L165-35b-Ig fusion was produced by transient transfection of COS as described for BSL2-4616811-Ig, below. BSL2-L165-35b-Ig fusion protein was purified using methods described herein. The concentration of the BSL2-L165-35b-Ig fusion protein was estimated by absorbance at 280 nm assuming an extinction coefficient of 1.4. The nucleotide and predicted amino acid sequence of BSL2-L165-35b-Ig (BLS2v1c2-Ig) is shown in **Figures 5A-5B**.

EXAMPLE 7: BSL2-L165-21-Ig (BSL2v2c2-Ig) fusion construct

PCR amplification of the BLS2-L165-21 cDNA template was performed using BSL2-L165-21-Ig-1 and BSL2-L165-21-Ig-2 primers (both primers described for the BSL2-4616811-Ig construction, below). The PCR reaction mixture included 42 µl GibcoBRL PCR Super Mix; 2 µl template (approximately 300 ng/µl; diluted 1:100); 2.5 µl of 1 pM/µl BSL2 L165-21 Ig-1 primer; 2.5 µl of 1 pM/µl BSL2 L165-21 Ig-2 primer; and 1 µl CLONTECH Advantage 2 DNA Polymerase mix. The PCR reaction was carried out as follows. The reaction mixture was incubated at 95°C for 5 min, followed by 35 cycles of incubation at 95°C for 45 sec, 58.5°C for 45 sec, and 72°C for 90

sec, followed by incubation at 72°C for 5 min. The reaction mixture was then held at 4°C.

Following this, the PCR product was cloned into a TA vector (Invitrogen; Cat. # K2000-01 and K2000-40) using the protocol provided by the manufacturer. The ligation reaction included 5 µl H_2O; 1 µl 10 X buffer (Roche, Mannheim, Germany); 2 µl vector pCR2.1; 1 µl PCR product (unpurified); and 1 µl T4 Ligase (Roche). One-half of the ligation mixture was used for transformation into max efficiency DH5α competent cells (Invitrogen) and plated as described, above. White colonies were isolated and grown in culture, and minipreps were performed (QIAGEN). The miniprep DNA and vector L200-1 (described herein) were digested with *Kpn*I and *Eco*RI in SuRE/Cut Buffer A (Boehringer Mannheim, Mannheim, Germany). The digestion mixture included 14 µl miniprep DNA or L200-1 vector; 2 µl *Kpn*I; 2 µl *Eco*RI; 2 µl 10 X Buffer A; and 10 µl dH_2O. The digestion mixture was electrophoresed on a 1% SeaPlaque Low Melt agarose gel (FMC, Rockland, ME). Bands of approximately 750-bp from the miniprep DNA and approximately 6200-bp from the L200-1 vector were excised and melted at 65°C.

Next, ligation reactions were carried out in 10 µl total volume. The ligation reactions included reagents listed in the table below.

	5:1 Insert:Vector	2:1 Insert:Vector	Control
Insert BSL2-L165-21	5 µl	2 µl	0 µl
Vector L200-1	1 µl	1 µl	1 µl
T4 Ligase (Roche)	1 µl	1 µl	1 µl
10 X Ligation Buffer (Roche)	1 µl	1 µl	1 µl
dH_2O	2 µl	5 µl	7 µl

Ligation reactions were incubated overnight at 14°C. After this, the ligation mixture was used for transformation into DH5α Max Efficiency Cells (Invitrogen). For transformations, 100 µl of cells were aliquotted into pre-chilled 14 ml snap cap tubes (Falcon, Becton Dickinson, Franklin Lakes,

NJ). Next, 2 µl of DNA was added to the cells, and cells were incubated on ice for 25-30 min. Cells were heat-shocked at 42°C for 45 sec, and then placed back on ice for at least 2 min. Following this, 900 µl of SOC growth medium (GibcoBRL) was added to each tube. The tubes were incubated for 1 hr at 37°C. After this, the cells were plated onto LB plates supplemented with 100 µg/ml ampicillin. Plates were then incubated at 37°C overnight.

Individual colonies were isolated and grown in 3 ml of LB growth medium supplemented with 100 µg/ml ampicillin. An initial miniprep was performed using a commercially available kit (QIAGEN, Valencia, CA; Cat. # 27106) to confirm insert orientation and sequence quality. All miniprep samples tested were shown to contain the correct insert orientation. After testing for sequence quality, a Plasmid Giga Prep kit (QIAGEN; Cat. # 12191) was used for large-scale production of DNA. For the Giga Prep, 2.5 L of culture was divided into three flasks. These flasks were incubated approximately 15 hr, but not longer 18 hr. Following this, a Giga Prep was performed according to the manufacturer's directions. The nucleotide and predicted amino acid sequence of BSL2-L165-21-Ig (BLS2v2c2-Ig) is shown in **Figures 6A-6B.**

EXAMPLE 8: BSL2-4616811-Ig (BSL2vcvc-Ig) fusion construct

To construct the BSL2-4616811-Ig (BSL2vcvc-Ig) plasmid, the BSL2-4616811 extracellular domain was PCR amplified from first strand cDNA (GibcoBRL Cat. # 11904-018). cDNA was prepared from RNA purified from THP1 cells stimulated with 100 ng/ml LPS for 2 hr. RNA was purified using Invitrogen FastTrack 2.0 (Cat. # K1593-02). The PCR reaction included 1 µl cDNA; 5 µl GibcoBRL 10 X PCR buffer; 1.5 µl of 25 mM $MgCl_2$; 1 µl of 10 mM dNTPs (Boehringer-Mannheim); 2.5 µl BSL2-L165-21-Ig-1 primer (10 pM/µl); 2.5 µl BSL2-L165-21-Ig-2 primer (10 pM/µl); 1 µl CLONTECH Advantage polymerase (Cat. # 8417-1); and 35.5 µl milliQ H_2O. The primers contained the following sequences: BSL2-L165-21-Ig-1: 5' gg ggt acc atg ctg cgt cgg cg 3' (**SEQ ID NO:46**); and BSL2-L165-21-Ig-2: 5' cg gaa ttc tgg ggg gaa tgt cat ag 3' (**SEQ ID NO:47**). PCR samples were incubated at 94°C for 1

min; followed by 35 cycles of incubation at 94°C for 30 sec, 59°C for 30 sec, and 72°C for 45 sec; followed by incubation at 72°C for 10 min.

Following this, 30 µl of the PCR reaction was run on a 1.2% agarose/0.5 X TBE gel. A band of approximately 1100-bp was excised and purified using QIAGEN Gel Extraction Kit (Cat. # 28704). One microliter of the purified PCR product (L254) was ligated into pCR2.1 using the TA cloning kit (Invitrogen; Cat. # K2050-01). Five microliters of the ligation mixture was used for transformation into MAX Efficiency DH5-alpha competent bacteria (GibcoBRL; Cat. # 18258-012), and transformants were plated onto LB plates containing 100 µg/ml ampicillin and 800 µg X-Gal. White colonies were inoculated into 5 ml LB broth containing 100 µg/ml ampicillin, and grown at 37°C for 18 hr. Plasmid DNA was purified with QIAGEN spin miniprep kit (Cat. # 27106). Plasmid DNA was digested with *Kpn*I and *Eco*RI. Plasmids containing inserts of about 1300-bp were sequenced using Applied Biosystems automated DNA sequencers (ABI 3700 capillary array sequencers). L254-7 was determined to contain wild-type BSL2-4616811 sequence.

The Fc portion of human IgG1 was PCR amplified from a BSL1-Ig plasmid (pD19:BSL1Ig), which was deposited with the American Type Culture Collection (ATCC, 10801 University Blvd., Manassas, VA 20110-2209 USA) in accordance with the Budapest Treaty, under ATCC Designation No. PTA-1992, on June 6, 2000. The PCR reaction mixture contained 0.001 µl BSL1-Ig, 5 µl GibcoBRL PCR buffer; 1.5 µl of 25 mM $MgCl_2$; 1 µl of 10 mM dNTPs (Boehringer-Mannheim); 2.5 µl Ig-1 primer (10 pM/µl) 2.5 µl BSL1Ig-2 primer (10 pM/µl); 1 µl CLONTECH Advantage polymerase; and 36 µl dH_2O. The primers contained the following sequences: IgG-1: 5' g gaa ttc gag ccc aaa tct tgt gac aa 3' (**SEQ ID NO:48**); and BSL1Ig-2: 5' gc gc tct aga tca ttt acc cgg aga cag g 3' (**SEQ ID NO:49**). PCR samples were incubated at 94°C for 1 min; followed by 25 cycles of incubation at 94°C for 30 sec, 59°C for 30 sec, and 72°C for 30 sec; followed by incubation at 72°C for 10 min.

Following this, 30 µl of the PCR reaction was run on a 1.2% agarose/0.5 X TBE gel. A band of about 700-bp was excised and purified

using QIAGEN Qiaquick gel extraction kit. Two microliters of the purified fragment (L174) was ligated into pCR2.1 using the TA cloning kit (Invitrogen). Five microliters of the ligation mixture was used for transformation into GibcoBRL MAX Efficiency DH5-alpha competent bacteria, and transformants were plated onto LB plates containing 100 μg/ml ampicillin and 800 μg X-gal. Plates were incubated for 18 hr at 37°C. White colonies were inoculated into 5 ml LB broth containing 100 μg/ml ampicillin and grown at 37°C for 18 hr. Plasmid DNA was prepared using QIAGEN Qiaprep spin miniprep kit. Plasmid DNA was digested with *Eco*RI and run on an agarose gel. Plasmids containing inserts of about 900-bp were sequenced. L174-3 was determined to contain wild-type human IgG1 Fc sequence.

L174-3 was digested with *Eco*RI/*Xba*I and separated on a 1.2% agarose/0.5 X TBE gel. A band of about 750-bp was excised and purified using QIAGEN gel extraction kit. Ten microliters of the purified fragment was run on an agarose gel next to a standard to obtain an estimate of the concentration. Approximately 20 ng of the *Eco*RI/*Xba*I fragment was ligated (Ligation 200) into 40 ng of *Eco*RI/*Xba*I digested pCDNA3.1+ vector (Invitrogen) using GibcoBRL high concentration T4 DNA ligase (5 U/μl) diluted in GibcoBRL T4 DNA ligase buffer. Five microliters of the ligation mixture was used for transformation into MAX Efficiency DH5-alpha competent bacteria (GibcoBRL), and transformants were plated onto LB plates containing 100 μg/ml ampicillin. Plates were incubated at 37°C for 18 hr. Colonies were inoculated into LB broth containing 100 μg/ml ampicillin. Plasmid DNA was purified using QIAGEN spin miniprep kit and sequenced. The L200-1 sequence was determined to be identical to the L174-3 sequence.

The L254-7 BSL2-4146811 construct was digested with *Kpn*I/*Eco*RI. A band of about 1300-bp was excised from a 1.2% agarose/0.5 X TBE gel and ligated into the L200-1 Fc construct digested with *Kpn*I/*Eco*RI. Five microliters of the ligation reaction was used for transformation into MAX Efficiency DH5-alpha cells and plated onto LB plates containing 100 μg/ml ampicillin. Colonies were grown, and plasmid DNA was purified as above. Plasmid DNA was digested with *Kpn*I/*Xba*I and separated on an agarose gel

as above. Plasmids containing a band of about 2-kb were sequenced as above. BSL2-4616811-Ig was determined to contain the wild-type BSL2-4616811 and wild-type human IgG1 sequences. The nucleotide and predicted amino acid sequence of BSL2-4616811-Ig (BSL2vcvc-Ig) is shown in **Figures 4A-4B**. Plasmids comprising BSL2vcvc-Ig, BSL2v1c2-Ig, or BSL2v2c2-Ig sequences were deposited as a mixture with the American Type Culture Collection (ATCC, 10801 University Blvd., Manassas, VA 20110-2209 USA) in accordance with the Budapest Treaty, under ATCC Designation No. PTA-4056, on February 8, 2002.

The BSL2 sequence information is summarized in **Table 2**. BSL2 sequence information was also disclosed in U.S. Application Serial No. 10/077,023, filed February 15, 2002. It is noted that the SEQ ID NOs have been revised for the present invention. The conversion chart for the SEQ ID NOs is shown in **Table 3**.

TABLE 2

Sequence Name	Nucleic Acid (NA) **SEQ ID NO:**	NA FIG NO.	Amino Acid (AA) **SEQ ID NO:**	AA FIG. NO.
BSL2-4616811 (BSL2vcvc)	1 and 2	1A and 1B	3	1C
BSL2-L165-21 (BSL2v2c2)	4	2A	5	2B
BSL2-L165-35b (BSL2v1c2)	6	3A	7	3B
BSL2-4616811-Ig (BSL2vcvc-Ig)	8	4A	9	4B
BSL2-L165-35b-Ig (BSL2v1c2-Ig)	10	5A	11	5B
BSL2-L165-21-Ig (BSL2v2c2-Ig)	12	6A	13	6B

TABLE 3

Sequence Name	PRESENT Nucleic Acid (NA) **SEQ ID NO:**	PRIOR Nucleic Acid (NA) **SEQ ID NO:**	PRESENT Amino Acid (AA) **SEQ ID NO:**	PRIOR Amino Acid (AA) **SEQ ID NO:**
BSL2-4616811 (BSL2vcvc)	1 and 2	6 and 131	3	7
BSL2-L165-21 (BSL2v2c2)	4	10	5	11
BSL2-L165-35b (BSL2v1c2)	6	12	7	13
BSL2-4616811-Ig (BSL2vcvc-Ig)	8	8	9	9
BSL2-L165-35b-Ig	10	132	11	133

Sequence Name	PRESENT Nucleic Acid (NA) SEQ ID NO:	PRIOR Nucleic Acid (NA) SEQ ID NO:	PRESENT Amino Acid (AA) SEQ ID NO:	PRIOR Amino Acid (AA) SEQ ID NO:
(BSL2v1c2-Ig)				
BSL2-L165-21-Ig (BSL2v2c2-Ig)	12	134	13	135

EXAMPLE 9: BSL2-4616811-Ig (BSL2vcvc-Ig) and BSL2-L165-35b (BSL2v1c2) construction for expression in CHO cells

The extracellular domain of human BSL2 containing either a vc (BSL2v1c2) or vcvc (BSL2vcvc) region was PCR amplified from cDNA and cloned into mammalian expression vector pD16 (described in U.S. Patent No. 6,051,228) using established methods (described by E. Kondri et al. (1997) *BioTechniques* 23(5): 830-833). The primers included a vcvc forward primer (5' act ata ggg aga ccc aag ctt ggt acc gga tcc atg ctg cgt cgg cgg ggc agc cct ggc 3'; **SEQ ID NO:**50); vcvc and v1c2 reverse primer (5' gtc aca aga ttt ggg ctc cgg atc ctc tgg ggg gaa tgt cat agg ctg ccc 3'; **SEQ ID NO:**51), and v1c2 forward primer (5' caa gct tgg tac cgg atc cat gga agc ccc agc tca gct tct ctt cct cct gct act ctg gct ccc aga tac cac cgg aac agg agc cct gga ggt cca g 3'; **SEQ ID NO:**52). The CHO vcvc construct incorporated the native signal peptide sequence and the CHO v1c2 construct incorporated the cd40 signal peptide sequence to direct the secretion of protein from mammalian cells. In addition, a stop codon was added to the end of the Ig sequence using a PCR primer.

The vector backbone was derived from the Invitrogen plasmid pcDNA3 and contained the following modifications. The neomycin resistance gene from pcDNA3 was replaced with the dihydrofolate reductase (DHFR) under control of the SV40 promoter missing the enhancer (also referred to as "weakened DHFR"). The SV40 promoter contained the SV40 origin of replication, so the vector could be used for transient expression of protein. The CMV promoter was used to express the fusion of interest, and the polyadenylation signal was obtained from the bovine growth hormone gene. The expression cassette for the fusion of interest was flanked by transcription termination sequences (i.e. 5' to the promoter and 3' to the poly(A)$^+$ site). The ampicillin resistance gene and ColE1 origin was included to allow plasmid

propagation in *E. coli*. All DNA fragments for cloning purposes were prepared by using standard molecular cloning methodologies (J. Sambrook (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories Press, Cold Spring Harbor, NY). The coding region was confirmed by DNA sequence analysis.

BSL2-Ig (BSL2vcvc-Ig or BSL2v1c2-Ig)-producing cell lines were generated by transfecting CHO DG44 cells (G. Urlaub et al. (1986) *Somat. Cell. Mol. Genet.* **12**(6):555-66) with an expression vector (pD16.hBSL2.Ig; either BSL2vcvc-Ig or BSL2v1c2-Ig) using a modified method of the high copy electroporation (J. Barsoum (1990) *DNA and Cell Biol.* 9:293-300; U.S. Patent No. 4,956,288). For electroporation, 200 μg of vector (pD16.hBSL2.Ig; either BSL2vcvc-Ig or BSL2v1c2-Ig) and sheared herring sperm DNA (as carrier) were co-precipitated with ethanol and resuspended in sterile PF CHO protein-free medium (JRH Biosciences, Lenexa, KS) CHO DG44 cells were obtained in exponential growth phase, and PF CHO was used as the electroporation medium. Cells were electroporated at 300 volts, 960 μF in a Bio-Rad gene pulser. Serum was omitted at all times during the process of cell line generation.

Following electroporation, cells were allowed to recover one day in non-selective media (PF CHO with 10 μg/ml recombinant insulin, 4 mM L-glutamine, 4 μg/ml hypoxantine, and 0.72 μg/ml thymidine). Cells were then seeded in 96-well plates at 250 or 1000 cells/well in selective media. Selective media was PF CHO with 10 μg/ml recombulin (recombinant insulin; GibcoBRL, Cat. # 28150-019), 4 mM L-glutamine, and 50 or 100 nM MTX (methotrexate). The plates were screened two weeks post-electroporation by ELISA for the selection of masterwells producing the highest level of BSL2-Ig (BSL2vcvc-Ig or BSL2v1c2-Ig) fusion protein. As used herein, a "masterwell" is a well containing transfected cells that have not been clonally isolated.

The cell lines (10 masterwells) expressing the highest levels of BSL2-Ig (BSL2vcvc-Ig or BSL2v1c2-Ig) were selected for further amplification. The cell lines were passed once per week through increasing concentrations of MTX (50 nM -> 100 nM -> 250 nM -> 500 nm). T-flasks were seeded at 2-5

x 10^4 cells/ml, depending on the cells' tolerance to the prior MTX level. Amplification was assessed by comparing titers of amplified and non-amplified masterwells in 7-day expression assays performed in 12-well tissue culture plates. Protein expression levels were assayed by enzyme linked immunosorbant assay (ELISA) and confirmed by SDS-PAGE (sodium dodecyl sulfate-polyacrylamide gel electrophoresis).

Fusion protein (BSL2vcvc-Ig or BSL2v1c2-Ig) was isolated by affinity purification using a protein A column. The protein was eluted from the column by five volumes of 0.1 M citrate pH 3, into one volume Tris pH 3. The eluted protein solution was dialyzed against PBS. To freeze transfected CHO cells, the culture was frozen while in exponential growth phase, as established by cell counts. The cultures showed high viability levels (> 9% by trypan blue exclusion).

EXAMPLE 10: BSL2 monoclonal antibodies

Purification of BSL2-Ig fusion protein: It is noted that the BSL2-4616811-Ig fusion protein used in the experiments that follow was isolated from COS cells, unless indicated otherwise. Purification of **BSL2-4616811-Ig** (human-IgG1) was accomplished by one-step affinity purification. Supernatant from transiently transfected COS cells expressing **BSL2-4616811-Ig** was applied to a Sepharose column of immobilized protein A. The column was washed with PBS until the absorbance at 280 nm reached the baseline level. Bound protein was eluted with ImmunoPure IgG Elution Buffer (Pierce Chemical, Rockford, IL; Cat. # 21004). Fractions containing the bound protein were neutralized with 1/8 v/v of 3 M sodium phosphate, pH 7. The resulting preparation was dialyzed against PBS, filtered (0.2 μm). All buffers contained 0.02% w/v sodium azide.

Immunization with **BSL2-4616811-Ig** polypeptide: For the initial immunization, mice between 1 and 3 months were used (BalbC; Harlan, Indianapolis, Indiana). RIBI adjuvant was prepared as follows. In one vial, 0.5 mg MPL (monophosphoryl lipid A; RIBI Immunochemical Research, Inc., Hamilton, MT); 0.5 mg TDM (synthetic trehalose dicorynomycolate; RIBI Immunochemical Research, Inc.); and 40 μl squalene with 0.2% Tween®80

were mixed together. The mixture was warmed to 40-45°C for 5-10 min, and 2 ml of **BSL2-4616811-Ig** polypeptide/PBS (125 µg/ml) was added. The solution was vortexed vigorously for several minutes. The solution was drawn into a syringe and injected immediately into the mice.

Dosages followed recommendations by RIBI Immunochemical Research, Inc. For the first injection, approximately 100 µg of **BSL2-4616811-Ig** polypeptide was resuspended in 250 µl of 1 X RIBI in PBS. The mixture was injected intraperitoneally with a 21 gauge needle. For second and later injections, boosts were given at least 3 weeks apart. Injections were at half dose. Four total boosts were given. At least 3 weeks following the **third boost**, once the titer reached an acceptable level (see below), the animal was given a final boost. For final injections, approximately 1 mg/ml of **BSL2-4616811-Ig** polypeptide was resuspended in PBS (RIBI was omitted), and the mixture was administered intravenously via tail veins. Animals were harvested 3-4 days later.

To monitor titer levels, sera samples were taken before initial immunization (background) and 7-10 days after each immunization for titer monitoring. Titer levels were measured by ELISA. Sera was harvested by eye-bleed or tail-bleed. Typically, 200 µl of blood was removed for sera testing.

Hybridoma cell lines: Hybridoma cell lines were constructed using the following reagents: Iscoves Modified Dulbecco's Medium (GibcoBRL; Cat. #12440-053); fetal bovine serum (Hyclone; Cat. # A-1115L, Lot # 11152564) heat inactivated for 30 min at 56°C; L-glutamine-200 mm, 100 X (GibcoBRL; Cat. # 25030-081); penicillin/streptomycin (GibcoBRL; Cat. # 15140-122); ORIGEN Hybridoma Cloning Factor (Igen International, Inc., Gaithersburg, MD; Cat. # IG50-0615, Lot #8077); HT Supplement 100 X (GibcoBRL; Cat. # 11067-030); HAT Supplement 100 X (GibcoBRL; Cat. # 31062-037); PEG 1500, (Boehringer Mannheim; Cat. # 783 641); Red Blood Cell Lysing Buffer from Lab Services (Cat. # 3KL-449); Trypan Blue; 70% ethanol; and myeloma cells (P3x) from ATCC.

The following equipment and supplies were used: laminar flow

hood; CO_2 incubator; inverted microscope; 37°C water bath; centrifuge; 96-well flat bottom tissue culture plates (Corning; Cat. # 25860-96); Serological pipettes and Integrid petri dishes (Falcon); 50 ml centrifuge tubes (Corning; Cat. # 430921); 15 ml conical tubes (Falcon; Cat. # 2096); autoclaved scissors and forceps; multichannel pipette; wide orifice 200 µl pipette tips (Denville Scientific, Inc., Metuchen, NJ; Cat. # P1105-CP); and sterile pipette tips (VWR, Buffalo Grove, IL; Cat. # 53508-794).

HAT and HT medium were made as follows:

HAT Medium		HT Medium	
IMDM	500 ml	IMDM	500 ml
L-Glutamine	2.5 ml	L-Glutamine	2.5 ml
Pen/Strep	5 ml	Pen/Strep	5 ml
HAT Supplement	5 ml	HT Supplement	5 ml
Origen Hy. Clon. F.	10% Final	Origen Hy. Clon. F.	10% Final

Mice were given a final boost 3-4 days prior to fusion in PBS intravenously or intraperitoneal. Myeloma cells were kept in exponential growth (log phase). The mice were euthanized, and the spleen from each mouse was aseptically harvested. The spleen was placed in a petri dish containing warm Iscoves solution without FBS. A spleen cell suspension was prepared and transferred to a centrifuge tube. HAT-sensitive myeloma cells were placed in a separate 50 ml centrifuge tube. Spleen cells and myeloma cells were centrifuged at 400 x g for 5 min, and the supernatant was aspirated. The red blood cells from the spleen were lysed with 5 ml RBC Lysing Buffer for 1 min, and the tube was filled with SF media (hybridoma serum-free media; GibcoBRL; Cat. # 12045-076). Splenocytes were washed with 50 ml SF media, and spleen cells and myeloma cells were centrifuged in separate centrifuge tubes at 400 x g for 5 min. Spleen cells and myeloma cells were counted and resuspended in 25 ml with SF media. Myeloma cells were added to spleen cells to give a 1:4 ratio. The mixture was centrifuged at 400 x g for 10 min to form a tight pellet, and all media solution was removed by aspiration.

For the cell fusion experiments, PEG, SF media, and HAT media were incubated at 37°C. One milliliter of 50% PEG was added to the

cells for 1 min (PEG was added for 30 sec and cells were stirred for 30 sec). The PEG solution was added to the side of the tube, and the pellet was gently stirred. With stirring, 1 ml SF media was added to the cells for 1 min, and 8 ml of SF media was added to the cells for 2 min. Cells were centrifuged at 400 x g for 10 min, and the supernatant was aspirated. Cells were gently resuspended in 10 ml HAT selective media by aiming pipette directly at pellet and stirring. Additional HAT media was added to bring cell concentration to 5 x 10^5 cells/ml. Cells were aliquotted into 96-well tissue culture plates at 5 x 10^4 cells/well. After 3 days, HT media was added at 100 µl/well. Approximately 10 days later, clones were tested for antibody production. Positive clones were expanded to one well of a 24-well plate. Positive clones were then re-tested, isotyped, and expanded to T25 (0.25 cm square tissue culture flask).

ELISA analysis: To test for positive clones, ELISA analysis was performed using the following reagents and supplies: carbonate/bicarbonate pH 9.6 (Sigma, St. Louis, MO; Cat. # C-3041) for coat; Immulon 2 ELISA plates (Dynex, Chantilly, VA; Cat. # 0110103455); 10 X PBS (GibcoBRL) made to 1 X concentration; wash buffer comprising Tween®20 (0.05% final concentration) in 1 X PBS; block buffer/sample diluent comprising wash buffer with 5% NFM non-fat milk; and chromogen mixture comprising 50% TMB (Kirkegaard & Perry Labs Gaithersburg, MD; Cat. # 50-76-01) and 50% peroxidase (Kirkegaard & Perry Labs Cat. # 50-65-00).

For ELISA, plates were coated with 75 µl/well (1 µg/ml) of **BSL2-4616811-Ig** in carbonate/bicarbonate overnight at 4°C. Plates were washed with PBS Tween®20 (using Skatron), and blocked with 300 µl block buffer for 45 min at room temperature. Plates were flicked dry and incubated with 75 µl/well sera diluted in blocking buffer (sera was diluted 1:50 for highest concentration and then serially diluted by factors of three) for 45 min at room temperature, and washed as before. Plates were then incubated with 75 µl/well anti-mouse IgG in blocking buffer (1:10000 dilution; HRP-labeled; Amersham Pharmacia Biotech, Piscataway, NJ) for 45 min at room temperature, and washed as before. Following this, plates were incubated

with 100 µl/well chromogen mixture, and incubated up to 15 min at room temperature. The signal was quenched with 100 µl 1N sulfuric acid, and samples were read at 450/630 nm. Using ELISA, supernatants from hybridomas were initially screened against of **BSL2-4616811-Ig** fusion protein, and then screened against Ig protein alone. Hybridomas that produced antibodies that bound to of **BSL2-4616811-Ig**, but not Ig, were designated as positive clones.

Subcloning: Positive clones from the initial fusion plate were expanded. Once growing, cells were put through two rounds of single cell cloning to ensure that they were monoclonal. Each hybridoma was plated in a 96-well tissue culture plate at a concentration of 0.5 cells/well or less. Once macroscopic colonies formed, supernatants were screened by ELISA. Positive clones from each hybridoma were titered by ELISA. The clones giving rise to the strongest signals were expanded and put through a second round of cloning. Positive clones were again screened by ELISA and titered. The clones giving rise to the strongest signal were expanded and frozen back.

Hybridoma cells producing anti-BSL2-1F7G2 MAb, anti-BLS2-3E6D3 MAb, anti-BSL2-4C2C6 MAb, or anti-BLS2-5D7E2 MAb were deposited with the American Type Culture Collection (ATCC, 10801 University Blvd., Manassas, VA 20110-2209 USA) in accordance with the Budapest Treaty, under ATCC Designation No. PTA-4058, PTA-4059, PTA-4060, and PTA-4057 respectively, on February 8, 2002.

EXAMPLE 11: FACS analysis of lung epithelial cells using BSL2 monoclonal antibodies

A549, a lung epithelium cell line was cultured in RPM1 1640 (GibcoBRL Cat. # 11875-005) plus 10% FBS (Summit, Ft Collins, CO; Cat. # S-100-05) and 1% penicillin-streptomycin (GibcoBRL Cat. # 15140-122) at 37°C in 5% CO_2 to 90% confluence in a T75 flask (Becton Dickinson, Franklin Lakes, NJ; Cat. # 353111). Cells were lifted with Versene (GibcoBRL Cat. # 15040-066) and washed twice in RPMI 1640. Cells were added to a 96-well plate (Becton Dickinson Cat. # 353077; 2.5 x 10^5 cells per well), and centrifuged at 2000 RPM in a Beckman tabletop centrifuge. Next, cells were

resuspended in RPMI 1640 or RPMI1640 with 1 μg negative control antibody (MAb 15E10AA3; also called MAb 15E10A3, MAb 3-13E10A3, or MAb 3_15) or hybridoma supernatant, and incubated on ice for 30 min. It is noted that MAb 15E10AA3 does not recognize the BSL2 polypeptides, but is the identical isotype as the anti-BSL2 antibodies. Cells were then washed twice in RPMI 1640, and resuspended in goat anti-mouse anti-Fc FITC conjugated antibodies (BioSource, Camarillo, CA; Cat. # AMI4408) diluted 1:50 in RPMI 1640. Following this, cells were incubated on ice for 30 min, washed twice in RPMI 1640, resuspended in RPMI 1640, and analyzed on a Becton Dickinson FACScan. Results of FACS analysis are shown for anti-BSL2-4616811 MAbs (**Figure 9**). It is noted that all MAbs bound to the A549 cells. It is also noted that anti-BSL2 MAb 1F7G2, anti-BSL2 MAb 2B10D7, anti-BSL2 MAb 3E6D3, anti-BSL2 MAb 4C2C6, and anti-BSL2 MAb 5D7E2 are also termed anti-BSL2-1 MAb, anti-BSL2-2 MAb, anti-BSL2-3 MAb, anti-BLS2-4 MAb, and anti-BSL2-5 MAb, respectively, as described herein.

EXAMPLE 12: Peripheral blood T Cell assays:

Peripheral blood T-cell assays were performed to determine the immunomodulatory properties of BSL2-4616811-Ig (BSL2vcvc-Ig), monclonal antibodies directed to BSL2-4616811, and BSL2-L165-35b-Ig (BSL2v1c2-Ig).

1. For the first set of experiments, 100 μl of the indicated concentration (2, 1, 0.5, 0.25, 0.13, or 0 μg/ml) of anti-CD3 MAb G19.4 (described herein) was added in triplicate to a Costar plate (Corning Inc., Corning NY; Cat. # 3595) in Gibco DPBS (Invitrogen Corp., Grand Island, NY). The plate was incubated at 4°C for 16 hr. The plate was washed two times in DPBS. Following this, 100 μl of 30 μg/ml BSL2-4616811-Ig (BSL2vcvc-Ig) or 10 μg/ml ChiL6 fusion protein was added per well in triplicate and incubated at 37°C for 4 hr. The plate was washed two times in DPBS. Then, 50,000 E-rosetted peripheral blood T-cells in 200 μl Gibco RPMI 1640 (Cat. # 11875-085) plus 1/100 volume Gibco penicillin-streptomycin (Cat. # 15140-122) plus 10% human serum (Sigma, St. Louis, MO; Cat. # H4522) were added per well. The plate was incubated at 37°C in 5% CO_2 for 2 days.

Following this, 50 µl of the same media and 1/50 volume of Perkin-Elmer ^{3}H-thymidine (Perkin-Elmer Life Sciences Inc., Boston, MA; Cat. # NET-027) was added per well. The plate was incubated at 37°C in 5% CO_2 for 16 hr. The plate was harvested on a Brandel harvester model CH-600 using a Packard plate (Packard, Meriden CT; Cat. # 6005174). Then, 40 µl Packard Microscint 20 (Cat. # 6013621) was added per well. The plate was counted on a Packard TopCount NXT. Data was analyzed using Microsoft Excel 97 (Microsoft, Redmond, WA). Four independent experiments were performed, each with cells isolated from two different donors. Representative results obtained with cells isolated from donor 100 are shown in **Figure 10A**.

2. The peripheral blood T-cells assay was performed as described in (1), except that a constant concentration (250 ng/ml) of anti-CD3 MAb G19.4 was used, and decreasing concentrations of BSL2-4616811-Ig (BSL2vcvc-Ig; 90, 30, 10, 3.3, 1.1, or 0 µg/ml) and ChiL6 (30, 10, 3.3, 1.1, 0.37, 0 µg/ml) fusion proteins were used. Two independent experiments were performed, each with cells isolated from two different donors. Representative results obtained with cells isolated from donor 82 are shown in **Figure 10B**.

3. The peripheral blood T-cells assay was performed as described in (1), except that 40 ng/ml anti-CD3 MAb G19.4 was used and the plate was incubated 37°C for 4 hr. The plate was washed twice in DPBS. Then, a decreasing concentration (100 µl of 2, 1, 0.5, 0.25, 0.13, or 0 µg/ml) of anti-CD28 MAb 9.3 (described herein) was added to each well. The plate was incubated at 4°C for 16 hr. The plate was washed twice in DPBS and 100 µl of 90 µg/ml BSL2-4616811-Ig (BSL2vcvc-Ig) or 30 µg/ml ChiL6 was added per well in triplicate. Four independent experiments were performed, each with cells from two different donors. Representative results obtained with cells isolated from donor 50 are shown in **Figure 10C**.

4. The peripheral blood T-cells assay was performed as described in (1), except that a constant concentration (200 ng/ml) of anti-CD3 MAb G19.4 was used, and a decreasing concentration of BSL2-4616811-Ig (BSL2vcvc-Ig; 120, 60, 30, 15, 7.5, or 0 µg/ml), BSL2-L165-35b-Ig (BSL2v1c2-Ig; 80, 40, 20, 10, 5, or 0 µg/ml) or ChiL6 (80, 40, 20, 10, 5, or 0

μg/ml) was added. Two independent experiments were performed, each with cells isolated from two different donors. Representative results obtained with cells isolated from donor 44 are shown in **Figure 10D**.

5. The peripheral blood T-cells assay was performed as described in (1), except that the plate was initially coated with 250 ng/ml anti-CD3 MAb G19.4. Following washes, the plate was coated with 30 μg/ml BSL2-4616811-Ig (BSL2vcvc-Ig). Following additional washes, anti-BSL2-1 MAb, anti-BSL2-5 MAb, or non-specific 3_15 MAb (also called MAb 3-15E10A3, MAb 15E10A3, and MAb 15E10AA3) was added at decreasing concentrations (54, 18, 9, 2.2, 0.74, or 0 μg/ml) in 100 μl media. T-cells were added in 100 μl media. Two independent experiments were performed, each with cells isolated from two different donors. Representative results obtained with cells isolated from donor 117 are shown in **Figure 10E**.

6. The peripheral blood T-cells assay was performed as described in (1), except that the plates were coated with a constant concentration (200 ng/ml) of anti-CD3 MAb G19.4. Following washes, the plate was coated with 30 μg/ml BSL2vcvc-Ig isolated from CHO cells (see above). Following additional washes, either anti-BSL2-1 MAb, anti-BSL2-2 MAb, anti-BSL2-3 MAb, anti-BSL2-4 MAb, or non-specific MAb 3_15 was added at decreasing concentrations (20, 10, 5, 2.5, 1.25, or 0 μg/ml) in 100 μl media. T-cells were added in 100 μl media. The final concentrations of the antibodies were 10, 5, 2.5, 1.25, 0.63, 0 μg/ml. Two independent experiments were performed, each with cells isolated from two different donors. Representative results obtained with cells isolated from donor 10 are shown in **Figure 10F**.

7. The peripheral blood T-cells assay was performed as described in (1), except that the plates were coated with a constant concentration (200 ng/ml) of anti-CD3 MAb G19.4. Following washes, the plate was coated with 30 μg/ml ChiL6 fusion protein. Following additional washes, either anti-BSL2-1 MAb or non-specific 3_15 MAb was added at decreasing concentrations (40, 20, 10, 5, 2.5, or 0 μg/ml), or no antibody was added, in 50 μl media. T-cells were added in 150 μl media. The final concentrations of the antibodies were 10, 5, 2.5, 1.25, 0.63, or 0 μg/ml. One experiment was performed with

cells isolated from two different donors. Representative results obtained with cells isolated from donor 12 are shown in **Figure 10G**.

8. The peripheral blood T-cells assay was performed as described in (1), except that the plates were coated with a constant concentration of 200 ng/ml anti-CD3 MAb G19.4. Following washes, the plate was coated with 30 µg/ml BSL2-L165-35b-Ig (BSL2v1c2-Ig). Following additional washes, anti-BSL2-1 MAb or non-specific 3_15 MAb was added at decreasing concentrations (20, 10, 5, 2.5, 1.25, or 0 µg/ml), or no antibody was added, in 100 µl media. T-cells were added in 100 µl media. The final concentration of the antibodies was 10, 5, 2.5, 1.25, 0.63 or 0 µg/ml. One experiment was performed with cells isolated from two different donors. Representative results obtained with cells isolated from donor 12 are shown in **Figure 10H**.

9. The peripheral blood T-cells assay was performed as described in (1), except that the plates were coated with a constant concentration (200 ng/ml) of anti-CD3 MAb G19.4. Following washes, the plate was coated with 30 µg/ml BSL2-4616811-Ig (BSL2vcvc-Ig) isolated from CHO cells (see above). Following additional washes, the plate was coated with decreasing concentrations (10, 5, 2.5, 1.25, 0.63, or 0 µg/ml) of anti-BSL2-1 MAb or non-specific 3_15 MAb, or no antibody was added. Following more washes, T-cells were added in 200 µl media. One experiment was performed with cells isolated from two different donors. Representative results obtained from cells isolated from donor 12 are shown in **Figure 10I**.

10. The peripheral blood T-cells assay was performed as described in (1), except that the plates were coated with a constant concentration (200 ng/ml) of anti-CD3 MAb G19.4. Following washes, the plate was coated with decreasing concentrations (10, 5, 2.5, 1.25, 0.63, or 0 µg/ml) of anti-BSL2-1 MAb or non-specific 3_15 MAb, or no antibody was added. Following additional washes, the plate was coated with 30 µg/ml BSL2-4616811-Ig (BS2vcvc-Ig) isolated from CHO cells (see above). Following more washes, T-cells were added in 200 µl media. One experiment was performed with cells isolated from two different donors. Representative results obtained from cells isolated from donor 12 are shown in **Figure 10J**.

The results of these assays are summarized as follows. In these experiments, BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein acted as a potent inhibitor of T-cell proliferation, even at relatively high concentrations of anti-CD3 MAb G19.4 (**Figure 10A**). The optimal inhibitory concentration of BSL2-4616811-Ig in a T-cell proliferation assay was approximately 90 µg/ml (**Figure 10B**). Moreover, BSL2-4616811-Ig-mediated inhibition of T-cell proliferation appears to be dominant over T-cell stimulation with anti-CD28 MAb 9.3 (**Figure 10C**). In contrast, BSL2-L-165-35b-Ig (BSL2v1c2-Ig) appears to have no effect on T-cell proliferation (**Figure 10D**).

Surprisingly, all five anti-BSL2 monoclonal antibodies (used as soluble reagents) also have a potent inhibitory effect on T-cell proliferation (**Figures 10E-10F**). The inhibitory effect of the BSL2 monoclonal antibodies requires the presence of the BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein (compare **Figure 10E** to **Figures 10G-10H**). In addition, the BSL2 monoclonal antibody anti-BSL2-1 is more effective at inhibition when soluble, than when bound to the plate, or when bound to the plate in the presence of BSL2-4616811-Ig (BSL2vcvc-Ig; compare **Figure 10E** to **Figures 10I-10J**).

From these experiments, it is clear that the BSL2-4616811-Ig (BSL2vcvc-Ig) fusion protein inhibits T-cell proliferation. Moreover, it appears that the BSL2-4616811-Ig fusion protein acts through a pathway that is dominant to the CD28 stimulatory pathway. Interestingly, BSL2 monoclonal antibodies act synergistically with the BSL2-4616811-Ig fusion protein in inhibiting T-cell proliferation. While not wishing to be bound by theory, the mechanism of this synergy may involve the signaling of anti-BSL2 (BSL2vcvc) MAbs through BSL2 present on T-cells, and the formation of a complex on T-cells that contains anti-BSL2 MAbs bound to endogenous BSL2 (BSL2vcvc) bound to endogenous BSL2 (BSL2vcvc) ligand, and plate-bound BSL2-Ig (BSL2vcvc-Ig) bound to endogenous BSL2 (BSL2vcvc) ligand. However, other mechanisms are also possible.

EXAMPLE 13: Mixed lymphocyte reactions

In the mixed lymphocyte reactions (MLR), 100,000 E-rosetted peripheral blood T-cells from donor 124 were mixed with 100,000 elutriated

peripheral blood monocytes (isolated as described above) from donor 051, and BSL2-4616811-Ig, CTLA4-Ig, or ChiL6 were added. Final concentrations were 90, 30, 10, 3.3, 1.1, or 0.37 μg/ml for BSL2-4616811-Ig (BSL2vcvc-Ig), 60, 20, 6.6, 2.2, 0.73, 0.24 μg/ml for CTLA4-Ig, or 30, 10, 3.3, 1.1, 0.36, 0.12 μg/ml for ChiL6. The final volume was 200 μl. A Falcon plate (Becton Dickinson, Franklin Lakes NJ; Cat. # 35-3077) was used. Media was made as described above. The plate was incubated 4 days at 37°C in 5% CO_2. The plate was labeled, harvested, counted and the data analyzed as indicated above. Results are shown in **Figure 11A**.

In a second set of experiments, the MLR was performed as described, except that final concentrations were 90, 45, 22.5, 11.25, 5.625, or 0 μg/ml for BSL2-4616811-Ig (BSL2vcvc-Ig), 60, 30, 15, 7.5, 3.75, or 0 μg/ml for BSL2-L165-35b-Ig (BSL2v1c2-Ig), or 30, 15, 7.5, 3.75, 1.875, or 0 μg/ml) ChiL6. Results are shown in **Figure 11B**. The results depicted in **Figures 11A-11B** support the results shown in **Figures 10C-10D**, described above. In particular, the experiments show that BSL2-4616811-Ig (BSL2vcvc-Ig)-mediated inhibition of T-cell proliferation appears to be dominant over T-cell stimulation through CD28 (**Figure 11A**), and that BSL2-L165-35b-Ig (BSL2v1c2-Ig) appears to have no effect on T-cell proliferation (**Figure 11B**).

Binding Comparison of Anti-BSL2 Monoclonal Antibodies to BSL2-4616811-Ig (BSL2vcvc-Ig) and BSL2-L165-35b-Ig (BSL2v1c2-Ig). Plates were coated with 1 μg/ml of BSL2-4616811-Ig (BSL2vcvc-Ig) or BSL2-L165-35b-Ig (BSL2v1c2-Ig) at 50 μl/well and incubated at 4°C overnight. Wells were aspirated and plates were blocked with 200 μl of 1% milk blocking solution (KPL; Cat. # 50-82-00). Plates were incubated at room temperature for 60 min. Plates were then washed with PBS containing 0.05% Tween®20 using four washes with 300 μl/well, and 2 sec between each wash (Program BMR1). Anti-BSL2-1 MAb, anti-BSL2-2 MAb, anti-BSL2-3 MAb, anti-BSL2-4 MAb, anti-BSL2-5, and negative control antibody 3_15 MAb were added (10 μg/ml; 50 μl/well) and plates were incubated at room temperature for 60 min. Plates were washed as described, and donkey anti-mouse IgG (H+L) HRP-conjugated secondary antibody (Jackson ImmunoResearch Laboratories, Inc.,

West Grove, PA) was added. Plates were incubated for 60 min at room temperature, and washed as before. Following this, 50 µl/well Develop Solution (DAKO Corp., Carprinteria, CA, Cat. # S1599) was added. Plates were incubated at room temperature for about 20 min. Stop Solution was then added (2.0 N sulfuric acid; 50 µl/well). Plates were read for absorbance at 405 nm. The results shown in **Figure 12** indicate that there was no significant difference between the binding of the anti-BSL2 monoclonal antibodies to BSL2-4616811-Ig (BSL2vcvc-Ig) or BSL2-L165-35b-Ig (BSL2v1c2-Ig).

EXAMPLE 14: Identification and Cloning of VH and VL Domains of Antibodies Directed Against the BSL2 Polypeptide

V_H and V_L domains may be identified and cloned from cell lines expressing an antibody directed against a BSL2 (e.g., **SEQ ID NO:3**, **SEQ ID NO:11**, or **SEQ ID NO:13**) epitope by performing PCR with V_H and V_L specific primers on cDNA template made from the antibody expressing cell lines. Briefly, RNA is isolated from the cell lines and used as a template for RT-PCR designed to amplify the V_H and V_L domains of the antibodies expressed by the EBV cell lines. Cells may be lysed using the TRIzol reagent (Life Technologies, Rockville, MD) and extracted with one-fifth volume of chloroform. After addition of chloroform, the solution is allowed to incubate at room temperature for 10 min, and then centrifuged at 14,000 rpm for 15 min at 4°C in a tabletop centrifuge. The supernatant is collected and RNA is precipitated using an equal volume of isopropanol. Precipitated RNA is pelleted by centrifuging at 14,000 rpm for 15 min at 4°C in a tabletop centrifuge.

Following centrifugation, the supernatant is discarded and the pellet is washed with 75% ethanol. Following the wash step, the RNA is centrifuged again at 800 rpm for 5 min at 4°C. The supernatant is discarded and the pellet allowed to air dry. RNA is the dissolved in DEPC water and heated to 60°C for 10 min. Quantities of RNA can be determined using optical density measurements. cDNA may be synthesized according to methods well-known in the art and/or described herein from 1.5 to 2.5

micrograms of RNA using reverse transciptase and random hexamer primers. cDNA is then used as a template for PCR amplification of V_H and V_L domains. Primers used to amplify V_H and V_L genes are shown in **Tables 4 and 5**, below.

TABLE 4

Primer Sequences Used to Amplify V_L domains

Primer name	Primer Sequence	SEQ ID NO:
Hu Vkappal – 5'	gacatccagatgacccagtctcc	53
Hu Vkappa2a – 5'	gatgttgtgatgactcagtctcc	54
Hu Vkappa2b – 5'	gatattgtgatgactcagtctcc	55
Hu Vkappa3 – 5'	gaaattgtgttgacgcagtctcc	56
Hu Vkappa4 – 5'	gacatcgtgatgacccagtctcc	57
Hu Vkappa5 – 5'	gaaacgacactcacgcagtctcc	58
Hu Vkappa6 – 5'	gaaattgtgctgactcagtctcc	59
Hu Vlambdal – 5'	cagtctgtgttgacgcagccgcc	60
Hu Vlambda2 – 5'	cagtctgccctgactcagcctgc	61
Hu Vlambda3 – 5'	tcctatgtgctgactcagccacc	62
Hu Vlambda3b – 5'	tcttctgagctgactcaggaccc	63
Hu Vlambda4 – 5'	cacgttatactgactcaaccgcc	64
Hu Vlambda5 – 5'	caggctgtgctcactcagccgtc	65
Hu Vlambda6 – 5'	aattttatgctgactcagccccca	66
Hu Jkappal – 3'	acgtttgatttccacctggtccc	67
Hu Jkappa2 – 3'	acgtttgatctccagcttggtccc	68
Hu Jkappa3 – 3'	acgtttgatatccactttggtccc	69
Hu Jkappa4 – 3'	acgtttgatctccaccttggtccc	70
Hu Jkappa5 – 3'	acgtttaatctccagtcgtgtccc	71
Hu Vlambdal – 3'	cagtctgtgttgacgcagccgcc	72
Hu Vlambda2 – 3'	cagtctgccctgactcagcctgc	73
Hu Vlambda3 – 3'	tcctatgtgctgactcagccacc	74
Hu Vlambda3b – 3'	tcttctgagctgactcaggaccc	75
Hu Vlambda4 – 3'	cacgttatactgactcaaccgcc	76
Hu Vlambda5 – 3'	caggctgtgctcactcagccgtc	77
Hu Vlambda6 – 3'	aattttatgctgactcagccccca	78

TABLE 5

Primer Sequences Used to Amplify V_H domains.

Primer name	Primer Sequence	SEQ ID NO:
Hu VH1 – 5'	caggtgcagctggtgcagtctgg	79
Hu VH2 – 5'	caggtcaacttaagggagtctgg	80
Hu VH3 – 5'	gaggtgcagctggtggagtctgg	81
Hu VH4 – 5'	caggtgcagctgcaggagtcggg	82
Hu VH5 – 5'	gaggtgcagctgttgcagtctgc	83
Hu VH6 – 5'	caggtacagctgcagcagtcagg	84

Primer name	Primer Sequence	SEQ ID NO:
Hu JH1 – 5'	tgaggagacggtgaccagggtgcc	85
Hu JH3 – 5'	tgaagagacggtgaccattgtccc	86
Hu JH4 – 5'	tgaggagacggtgaccagggttcc	87
Hu JH6 – 5'	tgaggagacggtgaccgtggtccc	88

Typically a PCR reaction makes use of a single 5' primer and a single 3' primer. At times, when the amount of available RNA template is limiting, or for greater efficiency, groups of 5' and/or 3' primers may be used. For example, all five VH-5' primers and all JH-3' primers may be used in a single PCR reaction. The PCR reaction is carried out in a 50 µl volume containing 1 X PCR buffer, 2 mM each dNTP, 0.7 U High Fidelity Taq polymerase, 5' primer mix, 3' primer mix, and 7.5 µl cDNA. The 5' and 3' primer mix of both V_H and V_L can be made by pooling together 22 pmole and 28 pmole, respectively, of each of the individual primers. PCR conditions include incubation at 96°C for 5 min; followed by 25 cycles of incubation at 94°C for 1 min, 50°C for 1 min, and 72°C for 1 min; followed by an extension cycle of 72°C for 10 min. After the reaction has been completed, sample tubes may be stored at 4°C.

PCR samples are then electrophoresed on a 1.3% agarose gel. DNA bands of the expected sizes (506-bp for V_H domains, and 344-bp for V_L domains) can be cut out of the gel and purified using methods well known in the art and/or described herein. Purified PCR products can be ligated into a PCR cloning vector (TA vector from Invitrogen Inc., Carlsbad, CA). Individual cloned PCR products can be isolated after transformation into *E. coli* and blue/white color selection. Cloned PCR products may then be sequenced using methods commonly known in the art and/or described herein.

The PCR bands containing the V_H domain and the V_L domains can also be used to create full-length Ig expression vectors. V_H and V_L domains can be cloned into vectors containing the nucleotide sequences of a heavy (e.g., human IgGl or human IgG4) or light chain (human kappa or human lambda) constant regions such that a complete heavy or light chain molecule could be expressed from these vectors when transfected into an appropriate host cell. Further, when cloned heavy and light chains are both

expressed in one cell line (from either one or two vectors), they can assemble into a complete functional antibody molecule that is secreted into the cell culture medium. Methods using polynucleotides encoding V_H and V_L antibody domain to generate expression vectors that encode complete antibody molecules are well known within the art.

As various changes can be made in the above compositions and methods without departing from the scope and spirit of the invention, it is intended that all subject matter contained in the above description, shown in the accompanying drawings, or defined in the appended claims be interpreted as illustrative, and not in a limiting sense.

The contents of all patents, patent applications, published articles, books, reference manuals, texts and abstracts cited herein are hereby incorporated by reference in their entirety to more fully describe the state of the art to which the present invention pertains.

WHAT IS CLAIMED IS:

1. An isolated nucleic fusion acid molecule encoding amino acid sequence SEQ ID NO:13.

2. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding amino acids 1-246 of SEQ ID NO:13; and b) a nucleotide sequence encoding amino acids 249-480 of SEQ ID NO:13.

3. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding amino acids 2-246 of SEQ ID NO:13; and b) a nucleotide sequence encoding amino acids 249-480 of SEQ ID NO:13.

4. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding amino acids 29-246 of SEQ ID NO:13; and b) a nucleotide sequence encoding amino acids 249-480 of SEQ ID NO:13.

5. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding at least 90 contiguous amino acids of SEQ ID NO:11; and b) a nucleotide sequence encoding amino acids 249-480 of SEQ ID NO:13.

6. An isolated nucleic acid fusion molecule comprising a) nucleotide sequence comprising nucleotides 1-738 of SEQ ID NO:12; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:12.

7. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence comprising nucleotides 4-738 of SEQ ID NO:12; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:12.

8. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence comprising nucleotides 85-738 of SEQ ID NO:12; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:12.

9. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence comprising at least 270 contiguous nucleotides of SEQ ID NO:10; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:12.

10. A vector comprising the nucleic acid fusion molecule according to any one of claims 1-9.

11. A host cell comprising the vector according to claim 10.

12. The host cell according to claim 11 which is selected from the group consisting of bacterial, yeast, insect, mammalian, and plant cells.

13. An isolated fusion polypeptide comprising amino acid sequence SEQ ID NO:13.

14. An isolated fusion polypeptide comprising a) amino acids 1-246 of SEQ ID NO:13; and b) amino acids 249-480 of SEQ ID NO:13.

15. An isolated fusion polypeptide comprising a) amino acids 2-246 of SEQ ID NO:13; and b) amino acids 249-480 of SEQ ID NO:13.

16. An isolated fusion polypeptide comprising a) amino acids 29-246 of SEQ ID NO:13; and b) amino acids 249-480 of SEQ ID NO:13.

17. An isolated fusion polypeptide comprising a) at least 90 contiguous amino acids of SEQ ID NO:11; and b) amino acids 249-480 of SEQ ID NO:13.

18. An isolated antibody that binds to the fusion polypeptide according to any one of claims 13-17.

19. The antibody according to claim 18 which is monoclonal.

20. A hybridoma cell which produces the antibody according to claim 19.

21. An isolated BSL2v2c2 nucleic acid fusion molecule corresponding to ATCC Deposit No. PTA-4056 , deposited February 8, 2002.

22. An isolated BSL2v2c2 fusion polypeptide encoded by the nucleic acid fusion molecule corresponding to ATCC Deposit No. PTA-4056, deposited February 8, 2002.

23. A host cell comprising the BSL2v2c2 nucleic acid fusion molecule corresponding to ATCC Deposit No. PTA-4056, deposited February 8, 2002.

24. An isolated nucleic fusion acid molecule encoding amino acid sequence SEQ ID NO:11.

25. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding amino acids 1-226 of SEQ ID NO:11; and b) a nucleotide sequence encoding amino acids 229-480 of SEQ ID NO:11.

26. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding amino acids 2-226 of SEQ ID NO:11; and b) a nucleotide sequence encoding amino acids 229-480 of SEQ ID NO:11.

27. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding amino acids 29-226 of SEQ ID NO:13; and b) a nucleotide sequence encoding amino acids 229-480 of SEQ ID NO:11.

28. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence encoding at least 170 contiguous amino acids of SEQ ID NO:13; and b) a nucleotide sequence encoding amino acids 229-480 of SEQ ID NO:11.

29. An isolated nucleic acid fusion molecule comprising a) nucleotide sequence comprising nucleotides 1-738 of SEQ ID NO:10; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:10.

30. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence comprising nucleotides 4-738 of SEQ ID NO:10; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:10.

31. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence comprising nucleotides 85-738 of SEQ ID NO:10; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:10.

32. An isolated nucleic acid fusion molecule comprising a) a nucleotide sequence comprising at least 410 contiguous nucleotides of SEQ ID NO:12; and b) a nucleotide sequence comprising nucleotides 745-1440 of SEQ ID NO:10.

33. A vector comprising the nucleic acid fusion molecule according to any one of claims 24-32.

34. A host cell comprising the vector according to claim 33.

35. The host cell according to claim 34 which is selected from the group consisting of bacterial, yeast, insect, mammalian, and plant cells.

36. An isolated fusion polypeptide comprising amino acid sequence SEQ ID NO:11.

37. An isolated fusion polypeptide comprising a) amino acids 1-226 of SEQ ID NO:11; and b) amino acids 229-480 of SEQ ID NO:11.

38. An isolated fusion polypeptide comprising a) amino acids 2-226 of SEQ ID NO:11; and b) amino acids 229-480 of SEQ ID NO:11.

39. An isolated fusion polypeptide comprising a) amino acids 29-226 of SEQ ID NO:11; and b) amino acids 229-480 of SEQ ID NO:11.

40. An isolated fusion polypeptide comprising a) at least 170 contiguous amino acids of SEQ ID NO:13; and b) amino acids 229-480 of SEQ ID NO:11.

41. An isolated antibody that binds to the fusion polypeptide according to the any one of claims 36-40.

42. The antibody according to claim 41 which is monoclonal.

43. A hybridoma cell which produces the antibody according to claim 42.

44. An isolated BSL2v1c2 nucleic acid fusion molecule corresponding to ATCC Deposit No. PTA-4056, deposited February 8, 2002.

45. An isolated BSL2v1c2 fusion polypeptide encoded by the nucleic acid fusion molecule corresponding to ATCC Deposit No. PTA-4056, deposited February 8, 2002.

46. A host cell comprising the BSL2v1c2 nucleic acid fusion molecule corresponding to ATCC Deposit No. PTA-4056, deposited February 8, 2002.

FIG. 1A-1

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1     attcggctcg agggcgactg agccaggctg ggccgcgtcc ctgagtccca
51    gagtcggcgc ggcgcggcag gggcagcctt ccaccacggg gagcccagct
101   gtcagccgcc tcacaggaag atgctgcgtc ggcggggcag ccctggcatg
151   ggtgtgcatg tgggtgcagc cctgggagca ctgtggttct gcctcacagg
201   agccctggag gtccaggtcc ctgaagaccc agtggtggca ctggtgggca
251   ccgatgccac cctgtgctgc tccttctccc ctgagcctgg cttcagcctg
301   gcacagctca acctcatctg gcagctgaca gataccaaac agctggtgca
351   cagctttgct gagggccagg accagggcag cgcctatgcc aaccgcacgg
401   ccctcttccc ggacctgctg gcacagggca acgcatccct gaggctgcag
451   cgcgtgcgtg tggcggacga gggcagcttc acctgcttcg tgagcatccg
501   ggatttcggc agcgctgccg tcagcctgca ggtggccgct ccctactcga
551   agcccagcat gaccctggag cccaacaagg acctgcggcc aggggacacg
601   gtgaccatca cgtgctccag ctaccagggc taccctgagg ctgaggtgtt
651   ctggcaggat gggcagggtg tgcccctgac tggcaacgtg accacgtcgc
701   agatggccaa cgagcagggc ttgtttgatg tgcacagcat cctgcgggtg
751   gtgctgggtg caaatggcac ctacagctgc ctggtgcgca accccgtgct
801   gcagcaggat gcgcacagct ctgtcaccat cacaccccag agaagcccca
851   caggagccgt ggaggtccag gtccctgagg acccggtggt ggccctagtg
901   ggcaccgatg ccaccctgcg ctgctccttc tcccccgagc ctggcttcag
951   cctggcacag ctcaacctca tctggcagct gacagacacc aaacagctgg
1001  tgcacagttt caccgaaggc cgggaccagg gcagcgccta tgccaaccgc
1051  acggccctct tcccggacct gctggcacaa ggcaatgcat ccctgaggct
1101  gcagcgcgtg cgtgtggcgg acgagggcag cttcacctgc ttcgtgagca
1151  tccgggattt cggcagcgct gccgtcagcc tgcaggtggc cgctccctac
1201  tcgaagccca gcatgaccct ggagcccaac aaggacctgc ggccagggga
1251  cacggtgacc atcacgtgct ccagctaccg gggctaccct gaggctgagg
1301  tgttctggca ggatgggcag ggtgtgcccc tgactggcaa cgtgaccacg
1351  tcgcagatgg ccaacgagca gggcttgttt gatgtgcaca gcgtcctgcg
1401  ggtggtgctg ggtgcgaatg gcacctacag ctgcctggtg cgcaaccccg
1451  tgctgcagca ggatgcgcac ggctctgtca ccatcacagg gcagcctatg
1501  acattccccc cagaggccct gtgggtgacc gtggggctgt ctgtctgtct
1551  cattgcactg ctggtggccc tggcttcgt gtgctggaga aagatcaaac
1601  agagctgtga ggaggagaat gcaggagctg aggaccagga tggggaggga
1651  gaaggctcca agacagccct gcagcctctg aaacactctg acagcaaaga
1701  agatgatgga caagaaatag cctgaccatg aggaccaggg agctgctacc
1751  cctccctaca gctcctaccc tctggctgca atggggctgc actgtgagcc
1801  ctgcccccaa cagatgcatc ctgctctgac aggtgggctc cttctccaaa
1851  ggatgcgata cacagaccac tgtgcagcct tatttctcca atggacatga
1901  ttcccaagtc atcctgctgc ctttttttctt atagacacaa tgaacagacc
1951  acccacaacc ttagttctct aagtcatcct gcctgctgcc ttatttcaca
2001  gtacatacat ttcttaggga cacagtacac tgaccacatc accaccctct
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FIG. 1A-2

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2051  tcttccagtg ctgcgtggac catctggctg ccttttttct ccaaaagatg
2101  caatattcag actgactgac cccctgcctt atttcaccaa agacacgatg
2151  catagtcacc ccggccttgt ttctccaatg gccgtgatac actagtgatc
2201  atgttcagcc ctgcttccac ctgcatagaa tcttttcttc tcagacaggg
2251  acagtgcggc ctcaacatct cctggagtct agaagctgtt tcctttcccc
2301  tccttcctcc tcttgctcta gccttaatac tggccttttc cctccctgcc
2351  ccaagtgaag acagggcact ctgcgcccac cacatgcaca gctgtgcatg
2401  gagacctgca ggtgcacgtg ctggaacacg tgtggttccc ccctggccca
2451  gcctcctctg cagtgcccct ctcccctgcc catcctcccc acggaagcat
2501  gtgctggtca cactggttct ccaggggtct gtgatggggc ccctgggggt
2551  cagcttctgt ccctctgcct tctcacctct ttgttccttt cttttcatgt
2601  atccattcag ttgatgttta ttgagcaact acagatgtca gcactgtgtt
2651  aggtgctggg ggccctgcgt gggaagataa agttcctccc tcaaggactc
2701  cccatccagc tgggagacag acaactaact acactgcacc ctgcggtttg
2751  caggggggctc ctgcctggct ccctgctcca cacctcctct gtggctcaag
2801  gcttcctgga tacctcaccc ccatcccacc cataattctt acccagagca
2851  tggggttggg gcggaaacct ggagagaggg acatagcccc tcgccacggc
2901  tagagaatct ggtggtgtcc aaaatgtctg tccaggtgtg ggcaggtggg
2951  caggcaccaa ggcccctctgg acctttcata gcagcagaaa aggcagagcc
3001  tggggcaggg cagggccagg aatgctttgg ggacaccgag gggactgccc
3051  cccaccccca ccatggtgct attctggggc tggggcagtc ttttcctggc
3101  ttgcctctgg ccagctcctg gcctctggta gagtgagact tcagacgttc
3151  tgatgccttc cggatgtcat ctctccctgc cccaggaatg gaagatg
```

FIG. 1B

```
   1  atgctgcgtc ggcggggcag ccctggcatg ggtgtgcatg tgggtgcagc
  51  cctgggagca ctgtggttct gcctcacagg agccctggag gtccaggtcc
 101  ctgaagaccc agtggtggca ctggtgggca ccgatgccac cctgtgctgc
 151  tccttctccc ctgagcctgg cttcagcctg gcacagctca acctcatctg
 201  gcagctgaca gataccaaac agctggtgca cagctttgct gagggccagg
 251  accagggcag cgcctatgcc aaccgcacgg ccctcttccc ggacctgctg
 301  gcacagggca acgcatccct gaggctgcag cgcgtgcgtg tggcggacga
 351  gggcagcttc acctgcttcg tgagcatccg ggattttcggc agcgctgccg
 401  tcagcctgca ggtggccgct ccctactcga agcccagcat gaccctggag
 451  cccaacaagg acctgcggcc aggggacacg gtgaccatca cgtgctccag
 501  ctaccagggc taccctgagg ctgaggtgtt ctggcaggat gggcagggtg
 551  tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc
 601  ttgtttgatg tgcacagcat cctgcgggtg gtgctgggtg caaatggcac
 651  ctacagctgc ctggtgcgca accccgtgct gcagcaggat gcgcacagct
 701  ctgtcaccat cacacccag agaagcccca caggagccgt ggaggtccag
 751  gtccctgagg acccggtggt ggccctagtg ggcaccgatg ccaccctgcg
 801  ctgctccttc tcccccgagc ctggcttcag cctggcacag ctcaacctca
 851  tctggcagct gacagacacc aaacagctgg tgcacagttt caccgaaggc
 901  cgggaccagg gcagcgccta tgccaaccgc acggccctct tcccggacct
 951  gctggcacaa ggcaatgcat ccctgaggct gcagcgcgtg cgtgtggcgg
1001  acgagggcag cttcacctgc ttcgtgagca tccgggattt cggcagcgct
1051  gccgtcagcc tgcaggtggc cgctccctac tcgaagccca gcatgaccct
1101  ggagcccaac aaggacctgc ggccagggga cacggtgacc atcacgtgct
1151  ccagctaccg gggctaccct gaggctgagg tgttctggca ggatgggcag
1201  ggtgtgcccc tgactggcaa cgtgaccacg tcgcagatgg ccaacgagca
1251  gggcttgttt gatgtgcaca gcgtcctgcg ggtggtgctg ggtgcgaatg
1301  gcacctacag ctgcctggtg cgcaaccccg tgctgcagca ggatgcgcac
1351  ggctctgtca ccatcacagg gcagcctatg acattccccc cagaggccct
1401  gtgggtgacc gtggggctgt ctgtctgtct cattgcactg ctggtggccc
1451  tggctttcgt gtgctggaga aagatcaaac agagctgtga ggaggagaat
1501  gcaggagctg aggaccagga tggggaggga gaaggctcca agacagccct
1551  gcagcctctg aaacactctg acagcaaaga agatgatgga caagaaatag
1601  cc
```

FIG. 1C

```
1    MLRRRGSPGM GVHVGAALGA LWFCLTGALE VQVPEDPVVA LVGTDATLCC
51   SFSPEPGFSL AQLNLIWQLT DTKQLVHSFA EGQDQGSAYA NRTALFPDLL
101  AQGNASLRLQ RVRVADEGSF TCFVSIRDFG SAAVSLQVAA PYSKPSMTLE
151  PNKDLRPGDT VTITCSSYQG YPEAEVFWQD GQGVPLTGNV TTSQMANEQG
201  LFDVHSILRV VLGANGTYSC LVRNPVLQQD AHSSVTITPQ RSPTGAVEVQ
251  VPEDPVVALV GTDATLRCSF SPEPGFSLAQ LNLIWQLTDT KQLVHSFTEG
301  RDQGSAYANR TALFPDLLAQ GNASLRLQRV RVADEGSFTC FVSIRDFGSA
351  AVSLQVAAPY SKPSMTLEPN KDLRPGDTVT ITCSSYRGYP EAEVFWQDGQ
401  GVPLTGNVTT SQMANEQGLF DVHSVLRVVL GANGTYSCLV RNPVLQQDAH
451  GSVTITGQPM TFPPEALWVT VGLSVCLIAL LVALAFVCWR KIKQSCEEEN
501  AGAEDQDGEG EGSKTALQPL KHSDSKEDDG QEIA
```

FIG. 2A

```
1    atgctgcgtc ggcggggcag ccctggcatg ggtgtgcatg tgggtgcagc
51   cctgggagca ctgtggttct gcctcacagg agccctggag gtccaggtcc
101  ctgaagaccc agtggtggca ctggtgggca ccgatgccac cctgcgctgc
151  tccttctccc ccgagcctgg cttcagcctg gcacagctca acctcatctg
201  gcagctgaca gacaccaaac agctggtgca cagtttcacc gaaggccggg
251  accagggcag cgcctatgcc aaccgcacgg ccctcttccc ggacctgctg
301  gcacaaggca atgcatccct gaggctgcag cgcgtgcgtg tggcggacga
351  gggcagcttc acctgcttcg tgagcatccg ggatttcggc agcgctgccg
401  tcagcctgca ggtggccgct cctactcga agcccagcat gaccctggag
451  cccaacaagg acctgcggcc aggggacacg gtgaccatca cgtgctccag
501  ctaccggggc taccctgagg ctgaggtgtt ctggcaggat gggcagggtg
551  tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc
601  ttgtttgatg tgcacagcgt cctgcgggtg gtgctgggtg cgaatggcac
651  ctacagctgc ctggtgcgca accccgtgct gcagcaggat gcgcacggct
701  ctgtcaccat cacagggcag cctatgacat tccccccaga ggccctgtgg
751  gtgaccgtgg ggctgtctgt ctgtctcatt gcactgctgg tggccctggc
801  tttcgtgtgc tggagaaaga tcaaacagag ctgtgaggag gagaatgcag
851  gagctgagga ccaggatggg gagggagaag gctccaagac agccctgcag
901  cctctgaaac actctgacag caaagaagat gatggacaag aaatagcctg
951  a
```

FIG. 2B

```
1    MLRRRGSPGM GVHVGAALGA LWFCLTGALE VQVPEDPVVA LVGTDATLRC
51   SFSPEPGFSL AQLNLIWQLT DTKQLVHSFT EGRDQGSAYA NRTALFPDLL
101  AQGNASLRLQ RVRVADEGSF TCFVSIRDFG SAAVSLQVAA PYSKPSMTLE
151  PNKDLRPGDT VTITCSSYRG YPEAEVFWQD GQGVPLTGNV TTSQMANEQG
201  LFDVHSVLRV VLGANGTYSC LVRNPVLQQD AHGSVTITGQ PMTFPPEALW
251  VTVGLSVCLI ALLVALAFVC WRKIKQSCEE ENAGAEDQDG EGEGSKTALQ
301  PLKHSDSKED DGQEIA*
```

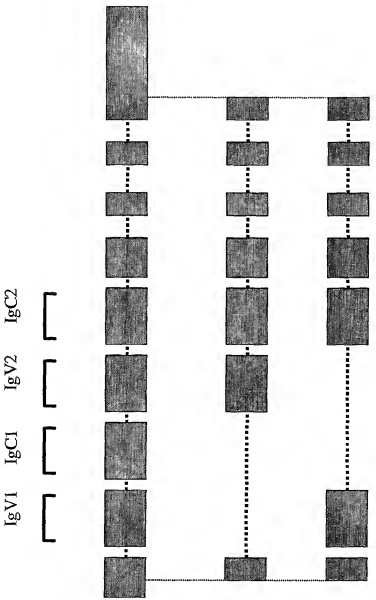
FIG. 3A

```
1    atgctgcgtc ggcggggcag ccctggcatg ggtgtgcatg tgggtgcagc
51   cctgggagca ctgtggttct gcctcacagg agccctggag gtccaggtcc
101  ctgaagaccc agtggtggca ctggtgggca ccgatgccac cctgtgctgc
151  tccttctccc ctgagcctgg cttcagcctg gcacagctca acctcatctg
201  gcagctgaca gataccaaac agctggtgca cagctttgct gagggccagg
251  accagggcag cgcctatgcc aaccgcacgg ccctcttccc ggacctgctg
301  gcacaaggca atgcatccct gaggctgcag cgcgtgcgtg tggcggacga
351  gggcagcttc acctgcttcg tgagcatccg ggatttcggc agcgctgccg
401  tcagcctgca ggtggccgct ccctactcga agcccagcat gaccctggag
451  cccaacaagg acctgcggcc aggggacacg gtgaccatca cgtgctccag
501  ctaccggggc taccctgagg ctgaggtgtt ctggcaggat gggcagggtg
551  tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc
601  ttgtttgatg tgcacagcgt cctgcgggtg gtgctgggtg cgaatggcac
651  ctacagctgc ctggtgcgca accccgtgct gcagcaggat gcgcacggct
701  ctgtcaccat cacagggcag cctatgacat tccccccaga ggccctgtgg
751  gtgaccgtgg ggctgtctgt ctgtctcatt gcactgctgg tggccctggc
801  tttcgtgtgc tggagaaaga tcaaacagag ctgtgaggag gagaatgcag
851  gagctgagga ccaggatggg gagggagaaa gctccaagac agccctgcag
901  cctctgaaac actctgacag caaagaagat gatggacaag aaatagcctga
```

FIG. 3B

```
1    MLRRRGSPGM GVHVGAALGA LWFCLTGALE VQVPEDPVVA LVGTDATLCC
51   SFSPEPGFSL AQLNLIWQLT DTKQLVHSFA EGQDQGSAYA NRTALFPDLL
101  AQGNASLRLQ RVRVADEGSF TCFVSIRDFG SAAVSLQVAA PYSKPSMTLE
151  PNKDLRPGDT VTITCSSYRG YPEAEVFWQD GQGVPLTGNV TTSQMANEQG
201  LFDVHSVLRV VLGANGTYSC LVRNPVLQQD AHGSVTITGQ PMTFPPEALW
251  VTVGLSVCLI ALLVALAFVC WRKIKQSCEE ENAGAEDQDG EGESSKTALQ
301  PLKHSDSKED DGQEIA
```

FIG. 3C



A: cDNA BSL2vcvc (BSL2-4616811)
B: cDNA BSL2v2c2 (BSL2-L165-21)
C: cDNA BSL2v1c2 (BSL2-L165-35b)

FIG. 4A

```
   1  atgctgcgtc ggcggggcag ccctggcatg ggtgtgcatg tgggtgcagc
  51  cctgggagca ctgtggttct gcctcacagg agccctggag gtccaggtcc
 101  ctgaagaccc agtggtggca ctggtgggca ccgatgccac cctgtgctgc
 151  tccttctccc ctgagcctgg cttcagcctg gcacagctca acctcatctg
 201  gcagctgaca gataccaaac agctggtgca cagctttgct gagggccagg
 251  accagggcag cgcctatgcc aaccgcacgg ccctcttccc ggacctgctg
 301  gcacagggca acgcatccct gaggctgcag cgcgtgcgtg tggcggacga
 351  gggcagcttc acctgcttcg tgagcatccg ggatttcggc agcgctgccg
 401  tcagcctgca ggtggccgct ccctactcga agcccagcat gaccctggag
 451  cccaacaagg acctgcggcc aggggacacg gtgaccatca cgtgctccag
 501  ctaccagggc taccctgagg ctgaggtgtt ctggcaggat gggcagggtg
 551  tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc
 601  ttgtttgatg tgcacagcat cctgcgggtg gtgctgggtg caaatggcac
 651  ctacagctgc ctggtgcgca accccgtgct gcagcaggat gcgcacagct
 701  ctgtcaccat cacaccccag agaagcccca caggagccgt ggaggtccag
 751  gtccctgagg acccggtggt ggccctagtg ggcaccgatg ccaccctgcg
 801  ctgctccttc tcccccgagc ctggcttcag cctggcacag ctcaacctca
 851  tctggcagct gacagacacc aaacagctgg tgcacagttt caccgaaggc
 901  cgggaccagg gcagcgccta tgccaaccgc acggccctct tcccggacct
 951  gctggcacaa ggcaatgcat ccctgaggct gcagcgcgtg cgtgtggcgg
1001  acgagggcag cttcacctgc ttcgtgagca tccgggattt cggcagcgct
1051  gccgtcagcc tgcaggtggc cgctccctac tcgaagccca gcatgaccct
1101  ggagcccaac aaggacctgc ggccagggga cacggtgacc atcacgtgct
1151  ccagctaccg gggctaccct gaggctgagg tgttctggca ggatgggcag
1201  ggtgtgcccc tgactggcaa cgtgaccacg tcgcagatgg ccaacgagca
1251  gggcttgttt gatgtgcaca gcgtcctgcg ggtggtgctg ggtgcgaatg
1301  gcacctacag ctgcctggtg cgcaaccccg tgctgcagca ggatgcgcac
1351  ggctctgtca ccatcacagg gcagcctatg acattccccc cagaattcga
1401  gcccaaatct tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg
1451  aactcctggg gggaccgtca gtcttcctct tcccccaaa acccaaggac
1501  accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt
1551  gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg
1601  aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg
1651  taccgtgtgg tcagcgtcct caccgtcctg caccaggact ggctgaatgg
1701  caaggagtac aagtgcaagg tctccaacaa agccctccca gccccatcg
1751  agaaaaccat ctccaaagcc aaagggcagc ccgagaacc acaggtgtac
1801  accctgcccc catcccggga tgagctgacc aagaaccagg tcagcctgac
1851  ctgcctggtc aaaggcttct atcccagcga catcgccgtg gagtgggaga
1901  gcaatgggca gccggagaac aactacaaga ccacgcctcc cgtgctggac
1951  tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag
2001  gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc
2051  acaaccacta cacgcagaag agcctctccc tgtctccggg taaatga
```

FIG. 4B

```
  1  MLRRRGSPGM GVHVGAALGA LWFCLTGALE VQVPEDPVVA LVGTDATLCC
 51  SFSPEPGFSL AQLNLIWQLT DTKQLVHSFA EGQDQGSAYA NRTALFPDLL
101  AQGNASLRLQ RVRVADEGSF TCFVSIRDFG SAAVSLQVAA PYSKPSMTLE
151  PNKDLRPGDT VTITCSSYQG YPEAEVFWQD GQGVPLTGNV TTSQMANEQG
201  LFDVHSILRV VLGANGTYSC LVRNPVLQQD AHSSVTITPQ RSPTGAVEVQ
251  VPEDPVVALV GTDATLRCSF SPEPGFSLAQ LNLIWQLTDT KQLVHSFTEG
301  RDQGSAYANR TALFPDLLAQ GNASLRLQRV RVADEGSFTC FVSIRDFGSA
351  AVSLQVAAPY SKPSMTLEPN KDLRPGDTVT ITCSSYRGYP EAEVFWQDGQ
401  GVPLTGNVTT SQMANEQGLF DVHSVLRVVL GANGTYSCLV RNPVLQQDAH
451  GSVTITGQPM TFPPEFEPKS CDKTHTCPPC PAPELLGGPS VFLPPPKPKD
501  TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST
551  YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY
601  TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD
651  SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPGK*
```

FIG. 5A

```
   1  atgctgcgtc ggcggggcag ccctggcatg ggtgtgcatg tgggtgcagc
  51  cctgggagca ctgtggttct gcctcacagg agccctggag gtccaggtcc
 101  ctgaagaccc agtggtggca ctggtgggca ccgatgccac cctgtgctgc
 151  tccttctccc ctgagcctgg cttcagcctg gcacagctca acctcatctg
 201  gcagctgaca gataccaaac agctggtgca cagctttgct gagggccagg
 251  accagggcag cgcctatgcc aaccgcacgg ccctcttccc ggacctgctg
 301  gcacaaggca atgcatccct gaggctgcag cgcgtgcgtg tggcggacga
 351  gggcagcttc acctgcttcg tgagcatccg ggatttcggc agcgctgccg
 401  tcagcctgca ggtggccgct ccctactcga agcccagcat gaccctggag
 451  cccaacaagg acctgcggcc aggggacacg gtgaccatca cgtgctccag
 501  ctaccggggc taccctgagg ctgaggtgtt ctggcaggat gggcagggtg
 551  tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc
 601  ttgtttgatg tgcacagcgt cctgcgggtg gtgctgggtg cgaatggcac
 651  ctacagctgc ctggtgcgca accccgtgct gcagcaggat gcgcacggct
 701  ctgtcaccat cacagggcag cctatgacat tcccccaga attcgagccc
 751  aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact
 801  cctgggggga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc
 851  tcatgatctc ccggaccct gaggtcacat gcgtggtggt ggacgtgagc
 901  cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt
 951  gcataatgcc aagacaaagc cgcgggagga gcagtacaac agcacgtacc
1001  gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag
1051  gagtacaagt gcaaggtctc caacaaagcc ctcccagcc ccatcgagaa
1101  aaccatctcc aaagccaaag ggcagccccg agaaccacag gtgtacaccc
1151  tgccccatc ccgggatgag ctgaccaaga accaggtcag ctgcgacctgc
1201  ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa
1251  tgggcagccg gagaacaact acaagaccac gcctcccgtg ctggactccg
1301  acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg
1351  cagcaggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa
1401  ccactacacg cagaagagcc tctccctgtc tccgggtaaa
```

FIG. 5B

```
   1  MLRRRGSPGM GVHVGAALGA LWFCLTGALE VQVPEDPVVA LVGTDATLCC
  51  SFSPEPGFSL AQLNLIWQLT DTKQLVHSFA EGQDQGSAYA NRTALFPDLL
 101  AQGNASLRLQ RVRVADEGSF TCFVSIRDFG SAAVSLQVAA PYSKPSMTLE
 151  PNKDLRPGDT VTITCSSYRG YPEAEVFWQD GQGVPLTGNV TTSQMANEQG
 201  LFDVHSVLRV VLGANGTYSC LVRNPVLQQD AHGSVTITGQ PMTFPPEFEP
 251  KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
 301  HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
 351  EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
 401  LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
 451  QQGNVFSCSV MHEALHNHYT QKSLSLSPGK
```

FIG. 6A

```
   1 atgctgcgtc ggcggggcag ccctggcatg ggtgtgcatg tgggtgcagc
  51 cctgggagca ctgtggttct gcctcacagg agccctggag gtccaggtcc
 101 ctgaagaccc agtggtggca ctggtgggca ccgatgccac cctgcgctgc
 151 tccttctccc ccgagcctgg cttcagcctg gcacagctca acctcatctg
 201 gcagctgaca gacaccaaac agctggtgca cagtttcacc gaaggccggg
 251 accagggcag cgcctatgcc aaccgcacgg cctcttccc ggacctgctg
 301 gcacaaggca atgcatccct gaggctgcag cgcgtgcgtg tggcggacga
 351 gggcagcttc acctgcttcg tgagcatccg ggatttcggc agcgctgccg
 401 tcagcctgca ggtggccgct ccctactcga agcccagcat gaccctggag
 451 cccaacaagg acctgcggcc aggggacacg gtgaccatca cgtgctccag
 501 ctaccggggc taccctgagg ctgaggtgtt ctggcaggat gggcagggtg
 551 tgcccctgac tggcaacgtg accacgtcgc agatggccaa cgagcagggc
 601 ttgtttgatg tgcacagcgt cctgcgggtg gtgctgggtg cgaatggcac
 651 ctacagctgc ctggtgcgca accccgtgct gcagcaggat gcgcacggct
 701 ctgtcaccat cacagggcag cctatgacat tcccccaga attcgagccc
 751 aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact
 801 cctgggggga ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc
 851 tcatgatctc ccggaccct gaggtcacat gcgtggtggt ggacgtgagc
 901 cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt
 951 gcataatgcc aagacaaagc cgcgggagga gcagtacaac agcacgtacc
1001 gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag
1051 gagtacaagt gcaaggtctc caacaaagcc ctcccagcc ccatcgagaa
1101 aaccatctcc aaagccaaag ggcagccccg agaaccacag gtgtacaccc
1151 tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc
1201 ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa
1251 tgggcagccg gagaacaact acaagaccac gcctcccgtg ctggactccg
1301 acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg
1351 cagcaggggа acgtcttctc atgctccgtg atgcatgagg ctctgcacaa
1401 ccactacacg cagaagagcc tctccctgtc tccgggtaaa
```

FIG. 6B

```
   1 MLRRRGSPGM GVHVGAALGA LWFCLTGALE VQVPEDPVVA LVGTDATLRC
  51 SFSPEPGFSL AQLNLIWQLT DTKQLVHSFT EGRDQGSAYA NRTALFPDLL
 101 AQGNASLRLQ RVRVADEGSF TCFVSIRDFG SAAVSLQVAA PYSKPSMTLE
 151 PNKDLRPGDT VTITCSSYRG YPEAEVFWQD GQGVPLTGNV TTSQMANEQG
 201 LFDVHSVLRV VLGANGTYSC LVRNPVLQQD AHGSVTITGQ PMTFPPEFEP
 251 KSCDKTHTCP PCPAPELLGG PSVFLFPPKP KDTLMISRTP EVTCVVVDVS
 301 HEDPEVKFNW YVDGVEVHNA KTKPREEQYN STYRVVSVLT VLHQDWLNGK
 351 EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSRDE LTKNQVSLTC
 401 LVKGFYPSDI AVEWESNGQP ENNYKTTPPV LDSDGSFFLY SKLTVDKSRW
 451 QQGNVFSCSV MHEALHNHYT QKSLSLSPGK
```

FIG. 7A-1

```
1     attcggctcg agggcgactg agccaggctg ggccgcgtcc ctgagtccca
51    gagtcggcgc ggcgcggcag gggcagcctt ccaccacggg gagcccagct
101   gtcagccgcc tcacaggaag atgctgcgtc ggcggggcag ccctggcatg
151   ggtgtgcatg tgggtgcagc cctgggagca ctgtggttct gcctcacagg
201   agccctggag gtccaggtcc ctgaagaccc agtggtggca ctggtgggca
251   ccgatgccac cctgtgctgc tccttctccc ctgagcctgg cttcagcctg
301   gcacagctca acctcatctg gcagctgaca gataccaaac agctggtgca
351   cagctttgct gagggccagg accagggcag cgcctatgcc aaccgcacgg
401   ccctcttccc ggacctgctg gcacagggca acgcatccct gaggctgcag
451   cgcgtgcgtg tggcggacga gggcagcttc acctgcttcg tgagcatccg
501   ggatttcggc agcgctgccg tcagcctgca ggtggccgct cctactcga
551   agcccagcat gaccctggag cccaacaagg acctgcggcc aggggacacg
601   gtgaccatca cgtgctccag ctaccagggc taccctgagg ctgaggtgtt
651   ctggcaggat gggcagggtg tgcccctgac tggcaacgtg accacgtcgc
701   agatggccaa cgagcagggc ttgtttgatg tgcacagcat cctgcgggtg
751   gtgctgggtg caaatggcac ctacagctgc ctggtgcgca acccgtgct
801   gcagcaggat gcgcacagct ctgtcaccat cacaccccag agaagcccca
851   caggagccgt ggaggtccag gtccctgagg acccggtggt ggccctagtg
901   ggcaccgatg ccaccctgcg ctgctccttc tccccgagc ctggcttcag
951   cctggcacag ctcaacctca tctggcagct gacagacacc aaacagctgg
1001  tgcacagttt caccgaaggc cgggaccagg gcagcgccta tgccaacccg
1051  acggccctct tcccggacct gctggcacaa ggcaatgcat ccctgaggct
1101  gcagcgcgtg cgtgtggcgg acgagggcag cttcacctgc ttcgtgagca
1151  tccgggattt cggcagcgct gccgtcagcc tgcaggtggc cgctccctac
1201  tcgaagccca gcatgaccct ggagcccaac aaggacctgc ggccagggga
1251  cacggtgacc atcacgtgct ccagctaccg gggctaccct gaggctgagg
1301  tgttctggca ggatgggcag ggtgtgcccc tgactggcaa cgtgaccacg
1351  tcgcagatgg ccaacgagca gggcttgttt gatgtgcaca gcgtcctgcg
1401  ggtggtgctg ggtgcgaatg gcacctacag ctgcctggtg cgcaacccg
1451  tgctgcagca ggatgcgcac ggctctgtca ccatcacagg gcagcctatg
1501  acattcccc cagaggccct gtgggtgacc gtgggctgct ctgtctgtct
1551  cattgcactg ctggtggccc tggctttcgt gtgctggaga aagatcaaac
1601  agagctgtga ggaggagaat gcaggagctg aggaccagga tggggaggga
1651  gaaggctcca agacagccct gcagcctctg aaacactctg acagcaaaga
1701  agatgatgga caagaaatag cctgaccatg aggaccaggg agctgctacc
1751  cctccctaca gctcctaccc tctggctgca atggggctgc actgtgagcc
1801  ctgcccccaa cagatgcatc ctgctctgac aggtgggctc cttctccaaa
1851  ggatgcgata cacagaccac tgtgcagcct tatttctcca atggacatga
1901  ttcccaagtc atcctgctgc ctttttttct atagacacaa tgaacagacc
1951  acccacaacc ttagttctct aagtcatcct gcctgctgcc ttatttcaca
2001  gtacatacat ttcttaggga cacagtacac tgaccacatc accacctct
2051  tcttccagtg ctgcgtggac catctggctg ccttttttct ccaaaagatg
```

FIG. 7A-2

```
2101  caatattcag actgactgac cccctgcctt atttcaccaa agacacgatg
2151  catagtcacc ccggccttgt ttctccaatg gccgtgatac actagtgatc
2201  atgttcagcc ctgcttccac ctgcatagaa tcttttcttc tcagacaggg
2251  acagtgcggc ctcaacatct cctggagtct agaagctgtt tcctttcccc
2301  tccttcctcc tcttgctcta gccttaatac tggccttttc cctccctgcc
2351  ccaagtgaag acagggcact ctgcgcccac cacatgcaca gctgtgcatg
2401  gagacctgca ggtgcacgtg ctggaacacg tgtggttccc ccctggccca
2451  gcctcctctg cagtgcccct ctcccctgcc catcctcccc acggaagcat
2501  gtgctggtca cactggttct ccaggggtct gtgatggggc ccctgggggt
2551  cagcttctgt ccctctgcct tctcacctct ttgttccttt cttttcatgt
2601  atccattcag ttgatgttta ttgagcaact acagatgtca gcactgtgtt
2651  aggtgctggg ggccctgcgt gggaagataa agttcctccc tcaaggactc
2701  cccatccagc tgggagacag acaactaact acactgcacc ctgcggtttg
2751  caggggggctc ctgcctggct ccctgctcca cacctcctct gtggctcaag
2801  gcttcctgga tacctcaccc ccatcccacc cataattctt acccagagca
2851  tggggttggg gcggaaacct ggagagaggg acatagcccc tcgccacggc
2901  tagagaatct ggtggtgtcc aaaatgtctg tccaggtgtg ggcaggtggg
2951  caggcaccaa ggccctctgg acctttcata gcagcagaaa aggcagagcc
3001  tggggcaggg cagggccagg aatgctttgg ggacaccgag gggactgccc
3051  cccaccccca ccatggtgct attctggggc tggggcagtc ttttcctggc
3101  ttgcctctgg ccagctcctg gcctctggta gagtgagact tcagacgttc
3151  tgatgccttc cggatgtcat ctctccctgc cccaggaatg gaagatg
```

FIG. 8A

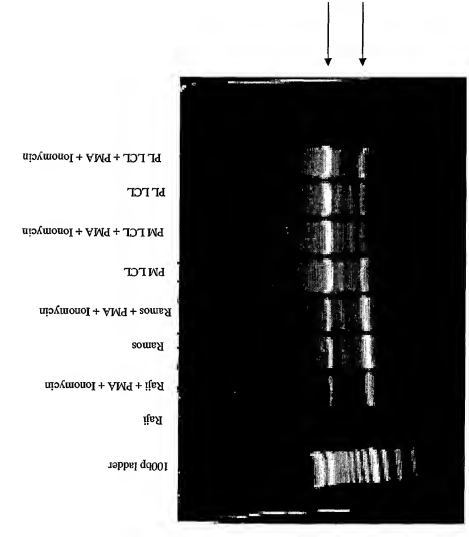

100bp ladder
Raji
Raji + PMA + Ionomycin
Ramos
Ramos + PMA + Ionomycin
PM LCL
PM LCL + PMA + Ionomycin
PL LCL
PL LCL + PMA + Ionomycin

FIG. 8C

100bp ladder
PBT 079 + PMA + Ionomycin
PBT 079 + 3x28
PBT 124
PBT 124 + PMA + Ionomycin

FIG. 8B

CE LCL
CE LCL + PMA + Ionomycin
HL60
HL60 + LPS
Thp1
Thp1 + LPS
HUVEC
HUVEC + TNF alpha 6hr
HUVEC + TNF alpha 24HR
100bp ladder

FIG. 8D

PBT 124 3x28
PBT 079
CEM
CEM + PMA + Ionomycin
Hut78
Hut78 + PMA + Ionomycin
100bp ladder

FIG. 8E

Lambda BstEII ladder
Clone 46168 11

FIG. 9

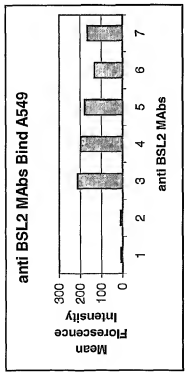


FIG. 10A

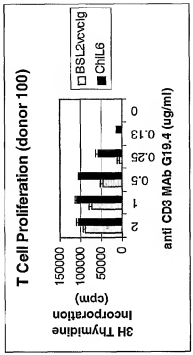


FIG. 10B

FIG. 10C

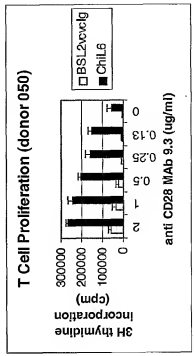


FIG. 10D

FIG. 10E

FIG. 10F

FIG. 10G

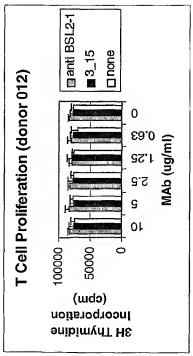


FIG. 10H

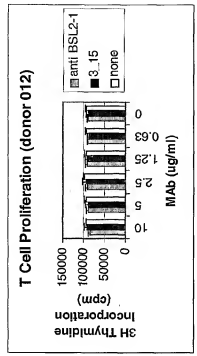


FIG. 10I

FIG. 10J

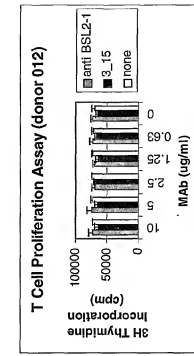


FIG. 11A

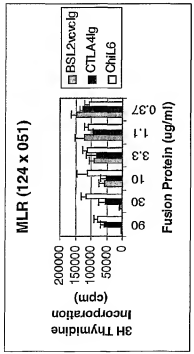


FIG. 11B

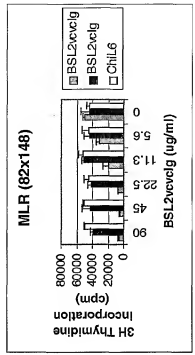


FIG. 12

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(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **MIKESELL, Glen, E.** [US/US]; 38 Bolton Road, Hamilton, NJ 08610 (US). **SHEN, Henry** [US/US]; 3 Bolton Circle, Princeton, NY 08540 (US).

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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*

(88) Date of publication of the international search report: 3 February 2005

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: B7-RELATED NUCLEIC ACIDS AND POLYPEPTIDES USEFUL FOR IMMUNOMODULATION

(57) Abstract: The present invention provides nucleic acids encoding B7-related factors that modulate the activation of immune or inflammatory response cells, such as T-cells. Also provided are expression vectors and fusion constructs comprising nucleic acids encoding B7-related polypeptides, including BSL2 and splice variants thereof. The present invention further provides isolated B7-related polypeptides that are specifically reactive with B7-related polypeptides, or portions thereof. In addition, the present invention provides assays utilizing B7-related nucleic acids, polypeptides, fusion proteins, or antibodies that are useful for diagnostic applications and the immunomodulation of a human or animal subject.

WO 2002/099119 A3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US02/18049

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/00, 15/09, 15/63; C07K 14/705, 16/28, 16/46;
US CL : 536/23.4, 23.5; 435/69.1, 252.3, 320.1; 530/350, 387.3, 388.22

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 536/23.4, 23.5; 435/69.1, 252.3, 320.1; 530/350, 387.3, 388.22

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 01/18021 A1 (HUMAN GENOME SCIENCES, INC.) 15 March 2001 (15.03.2001), see pages 1-6, 12-13, 26, 193-233, Figures 1-10 and SEQ ID NO:4.	1-20 and 24-43
Y	CHAPOVAL et al. B7-H3: A costimulatory molecule for T cell activation and IFN-g production. Nature Immunol. March 2001, Vol. 2. No. 3, pages 269-274, see entire document.	1-20 and 24-43

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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Date of the actual completion of the international search	Date of mailing of the international search report
09 December 2002 (09.12.2002)	10 FEB 2003
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Jessica H. Roark Telephone No. (703) 308-0196

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Continuation of B. FIELDS SEARCHED Item 3:
GenBank, WEST, Medline, CAPLUS, EMBASE, BIOSIS
Search terms: SEQ ID NOS: 10-13, B7-H3, Inventors' names